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STIC-Biotech/ChemLib

From: Seharaseyon, Jegatheesan
Sent: Monday, June 05, 2006 10:51 AM
To: STIC-Biotech/ChemLib
Subject: Re:10/063540

Please search SEQ ID NO: 34 in the pending and allowed databases.
Also please search with a word size of 6 amino acids.

Thanks

J. Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

- Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
- Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2006, 01:10:42 ; Search time 302 Seconds
(without alignments)
2076.691 Million cell updates/sec

Title: US-10-063-540-34
Perfect score: 3502
Sequence: 1 MRTVLTMKASVIMFLVL.....QYVPRITQICTFENSPRN 678

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------------|--------------------|
| 1 | 3502 | 100.0 | 678 | Q6UX17_HUMAN | Q6ux17 homo sapien |
| 2 | 3484.5 | 99.5 | 693 | Q9UDN0_HUMAN | Q9udn0 homo sapien |
| 3 | 3344 | 95.5 | 656 | Q96DRI_HUMAN | Q96dri homo sapien |
| 4 | 2826 | 80.7 | 650 | Q3RZ47_MOUSE | Q3rz47 mus musculu |
| 5 | 2823 | 80.6 | 650 | Q8VH15_MOUSE | Q8vh15 mus musculu |
| 6 | 2818 | 80.5 | 652 | Q95L12_BOVIN | Q95l12 bos taurus |
| 7 | 2801 | 80.0 | 650 | Q8K047_MOUSE | Q8k047 mus musculu |
| 8 | 2796 | 79.8 | 650 | Q9CY21_MOUSE | Q9cy21 mus musculu |
| 9 | 2682 | 76.6 | 628 | Q8B041_MOUSE | Q8b041 mus musculu |
| 10 | 2311.5 | 66.0 | 748 | Q5NTW9_CHICK | Q5ntw9 gallus gall |
| 11 | 1929 | 55.1 | 680 | Q4RP27_TETNG | Q4rp27 tetradon n |
| 12 | 1187.5 | 33.9 | 553 | Q8AW56_BRARE | Q8aw56 brachydanto |
| 13 | 1139 | 32.5 | 547 | COCH_CHICK | CO4163 gallus gall |
| 14 | 1129.5 | 32.3 | 550 | COCH_HUMAN | CO4405 homo sapien |
| 15 | 1123.5 | 32.1 | 550 | Q5EA64_BOVIN | Q5ea64 bos taurus |
| 16 | 1115 | 31.8 | 552 | Q3U0Z1_MOUSE | Q3u0z1 mus musculu |
| 17 | 1113 | 31.8 | 552 | COCH_MOUSE | Q62507 mus musculu |
| 18 | 1113 | 31.8 | 552 | Q3TAF5_MOUSE | Q3taf5 m activatd |
| 19 | 1017.5 | 29.1 | 494 | Q94I66_HUMAN | Q94i66 homo sapien |
| 20 | 1008.5 | 28.8 | 586 | Q4T252_TETNG | Q4t252 tetradon n |
| 21 | 848 | 24.2 | 203 | Q6P7T3_HUMAN | Q6p7t3 homo sapien |
| 22 | 834.5 | 23.8 | 401 | Q6ZP09_HUMAN | Q6zp09 homo sapien |
| 23 | 554 | 15.8 | 3124 | COCAI_CHICK | PI1944 gallus gall |
| 24 | 552 | 15.8 | 3119 | COCAI_MOUSE | Q60847 mus musculu |
| 25 | 543.5 | 15.5 | 3063 | COCAI_HUMAN | Q93715 homo sapien |
| 26 | 542.5 | 15.5 | 2884 | OSVVK2_HUMAN | OSVvk2 homo sapien |
| 27 | 542.5 | 15.5 | 3063 | OSVVK1_HUMAN | OSVvk1 homo sapien |
| 28 | 512 | 14.6 | 490 | Q7SYT5_XENLA | Q7syts xenopus lae |
| 29 | 505 | 14.4 | 490 | Q5BKH6_XENTR | Q5bkh6 xenopus tro |
| 30 | 504.5 | 14.4 | 3137 | CO6A3_CHICK | PI1989 gallus gall |
| 31 | 501.5 | 14.3 | 496 | MATN1_HUMAN | PI1941 homo sapien |

| | | | | | |
|----|-------|------|------|--------------|----------------------|
| 32 | 501.5 | 14.3 | 496 | Q5TB99_HUMAN | Q5tb99 homo sapien |
| 33 | 494.5 | 14.1 | 498 | Q5X124_RAT | Q5x124 ratu mus norv |
| 34 | 493 | 14.1 | 500 | Q8OVN5_MOUSE | Q8ovn5 mus musculu |
| 35 | 490 | 14.0 | 493 | MATN1_CHICK | P05099 gallus gall |
| 36 | 490 | 14.0 | 500 | MATN1_MOUSE | P51942 mus musculu |
| 37 | 488.5 | 13.9 | 1259 | Q4RP12_TETNG | Q4rp12 tetradon n |
| 38 | 485 | 13.8 | 507 | Q7ZVP3_BRARE | Q7zvp3 brachydanto |
| 39 | 478.5 | 13.7 | 644 | Q5NJU1_BRARE | Q5nj11 brachydanto |
| 40 | 471.5 | 13.5 | 2588 | Q53OF4_HUMAN | Q53of4 homo sapien |
| 41 | 471.5 | 13.5 | 3176 | CO6A3_HUMAN | PI2111 homo sapien |
| 42 | 466 | 13.3 | 3169 | Q4KKT6_CANFA | Q4kkt6 canis famli |
| 43 | 464 | 13.2 | 1453 | Q4RN11_TETNG | Q4rn11 tetradon n |
| 44 | 463 | 13.2 | 1182 | Q8C6K9_MOUSE | Q8c6k9 mus musculu |
| 45 | 459 | 13.1 | 685 | Q5NJJ2_BRARE | Q5nj12 brachydanto |

ALIGNMENTS

RESULT 1
ID Q6UX17_HUMAN PRELIMINARY: PRT: 678 AA.
AC Q6UX17;
BT 24-MAY-2005, integrated into UniprotKB/TREMBL.
DT 24-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE VIT.

GN ORFNames=UNQ647;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seahagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).

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CC
CC EMBL: AY358338; AAC08704.1; -; mRNA.
DR HSSP: Q43405; IUBI.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF03815; LCCL; 1.
DR Pfam: PF00092; VWA; 2.
DR PRINTS: PR00453; VWFADOMAIN.
DR SMART: SM00603; LCCL; 1.
DR SMART: SM00327; VWA; 2.
DR PROSITE: PS50820; LCCL; 1.
DR PROSITE: PS50234; VWF_A; 2.
SQ SEQUENCE 678 AA; 73530 MW; 9670E75A218C686C CRC64;

Query Match 100.0%; Score 3502; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 3e-219;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRTVLTMKASVIMFLVLVTGVHSNKEETAKKIKRPFYVPOINCQVKAAGKIIDPEFIV 60
DB 1 MRTVLTMKASVIMFLVLVTGVHSNKEETAKKIKRPFYVPOINCQVKAAGKIIDPEFIV 60

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QY 61 KCPAGCDDPKYHYGTDVYASYSVCGAAVHSGVLDSGGKILVRKYAGSGYKGSYNG 120
Db 61 KCPAGCDDPKYHYGTDVYASYSVCGAAVHSGVLDSGGKILVRKYAGSGYKGSYNG 120
QY 121 VQSLPRMRESFVLESKPKKGYTPSALTYSKSPAAQAGETTAKYGRPPIPGTTAAQ 180
Db 121 VQSLPRMRESFVLESKPKKGYTPSALTYSKSPAAQAGETTAKYGRPPIPGTTAAQ 180
QY 181 PVTLMQLLAVTAAVATPTTLPRPSPSAASTTSTIRPQSVGRSQDMDLMTATTTSSQNR 240
Db 181 PVTLMQLLAVTAAVATPTTLPRPSPSAASTTSTIRPQSVGRSQDMDLMTATTTSSQNR 240
QY 241 PRADPGIORODPSGAARQKPGAVSGLVYKEELSTQSLPVSIGDNCIDISFLIDG 300
Db 241 PRADPGIORODPSGAARQKPGAVSGLVYKEELSTQSLPVSIGDNCIDISFLIDG 300
QY 301 STSIGKRFRIOQLDLADVAQALDIPAPGLMGVVOYGDNDPAPHNLKHTNSRDLKTAI 360
Db 301 STSIGKRFRIOQLDLADVAQALDIPAPGLMGVVOYGDNDPAPHNLKHTNSRDLKTAI 360
QY 361 EKITRGGLSNVGAISFTYKNFSSKANGNSGAPNYYVWVDGMPDVKVEASRLARES 420
Db 361 EKITRGGLSNVGAISFTYKNFSSKANGNSGAPNYYVWVDGMPDVKVEASRLARES 420
QY 421 GINIFFTIEGAANEKQYVVEPNPANKAVCRNGFYSLHYQSFGHLKTLQPLVKRYCD 480
Db 421 GINIFFTIEGAANEKQYVVEPNPANKAVCRNGFYSLHYQSFGHLKTLQPLVKRYCD 480
QY 481 TDLRACSKTCLNSADIGFVIDSGSSVGTGNFRVYLQFVTNLTKPEISDTRIGAVOYT 540
Db 481 TDLRACSKTCLNSADIGFVIDSGSSVGTGNFRVYLQFVTNLTKPEISDTRIGAVOYT 540
QY 541 YEOGLFEGFDKYSKRPDIINAIRVGVWSSGTSFGAANFLEQLFKSKRNKMKMLLI 600
Db 541 YEOGLFEGFDKYSKRPDIINAIRVGVWSSGTSFGAANFLEQLFKSKRNKMKMLLI 600
QY 601 TDGASVDVIRPAAAHKGVITTAIGVAAAOELEVIAIHAPARDHSFDEDFDNLHQY 660
Db 601 TDGASVDVIRPAAAHKGVITTAIGVAAAOELEVIAIHAPARDHSFDEDFDNLHQY 660
QY 661 VPRIIQICTEFNSQPRN 678
Db 661 VPRIIQICTEFNSQPRN 678

RESULT 2
Q9UDNO HUMAN PRELIMINARY; PRT; 693 AA.
AC Q9UDNO; 096DW8;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 2.
DE Hypothetical protein VIT (Hypothetical protein FLJ32210).
GN Name=VIT;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cordes M., Kalicki J., Ames M.;
RT "the sequence of Homo sapiens BAC clone RP11-294L11.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

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RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura Y., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto K., Iwatsuki S., Iwatsuki S., Watanabe S., Hosoi T.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Iwihashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirao K., Ichida S.,
RA Ohtsuka T., Takiguchi S., Watanabe S., Yoshida M., Hoshino Y.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togaya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Mutsaers J., Yokoi H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshihawa Y., Matsunawa H., Ichihara T., Shihara T., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Hishigaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Taehiro H., Tanigami A., Fujitawa T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohnori Y.,
RA Kanabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtsuka T., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
RA Maksumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
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CC
CC EMBL: AK056772; BAB71279.1; -; mRNA.
CC EMBL: AC007363; AAF19243.2; -; genomic_DNA.
CC HSSP: O43405; IJBI.
CC HGNC: HGNC:12697; VIT.
CC InterPro: IPR004043; LCCL.
CC InterPro: IPR002035; VWF_A.
CC Pfam: PF03815; LCCL. 1.
CC Pfam: PF00092; VMA. 2.
CC PRINTS: PR00453; VWFADOMAIN.
CC SMART: SM00503; LCCL. 1.
CC SMART: SM00327; VMA. 2.
CC PROSITE: PS50820; LCCL. 1.
CC PROSITE: PS50234; VWF. 2.
CC KQ Hypothetical protein.
SQ SEQUENCE 693 AA; 75575 MW; 2DE8B2421F2D496D CRC64;

Query Match 99.5%; Score 3484.5; DB 2; Length 693;
Best Local Similarity 97.8%; Pred. No. 4.3e-218; Indels 15; Gaps 1;
Matches 678; Conservative 0; Mismatches 0;

QY 1 MRTVLTAKASVLEMFVLVLTGVSNSKETAKKIKPKFTVPQINCVDKAGKIIDEPIFV 60
Db 1 MRTVLTAKASVLEMFVLVLTGVSNSKETAKKIKPKFTVPQINCVDKAGKIIDEPIFV 60
QY 61 KCPAGCDDPKYHYGTDVYASYSVCGAAVHSGVLDSGGKILVRKYAGSGYKGSYNG 120
Db 61 KCPAGCDDPKYHYGTDVYASYSVCGAAVHSGVLDSGGKILVRKYAGSGYKGSYNG 120
QY 121 VQSLPRMRESFVLESKPKKGYTPSALTYSKSPAAQAGETTAKYGRPPIPGTTAAQ 180
Db 121 VQSLPRMRESFVLESKPKKGYTPSALTYSKSPAAQAGETTAKYGRPPIPGTTAAQ 180

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Db 121 VOSLSLPRWRESFVLESKPKKGVTPSPALTYSSSSKSPAAGETTKAYQRPPIGTTAAQ 180
Qy 181 PVTLMQLLAVTAAVATPTTLPRPSPAASTTSIPRPOSVGHRSQEMDLMSTATYSSQNR 240
Db 181 PVTLMQLLAVTAAVATPTTLPRPSPAASTTSIPRPOSVGHRSQEMDLMSTATYSSQNR 240
Qy 241 PRADPGIORODPSGAFOKPVGADVSL-----GLVPEKEELSTOSLEPVSL 285
Db 241 PRADPGIORODPSGAFOKPVGADVSLGEMDSWKPGSVLLDEGLVPKEELSTOSLEPVSL 300
Qy 286 GDPNCKIDSLFIDSTSGKRRFRIOKQLLDVAAQALDIPAGPLMGVVOYGDNPATHF 345
Db 301 GDPNCKIDSLFIDSTSGKRRFRIOKQLLDVAAQALDIPAGPLMGVVOYGDNPATHF 360
Qy 346 NLKHTNSRDLKTALEKITORGGLSNVGRASIFVTKNFPSKANGNSGAPNVVVVWDGM 405
Db 361 NLKHTNSRDLKTALEKITORGGLSNVGRASIFVTKNFPSKANGNSGAPNVVVVWDGM 420
Qy 406 PTDKVEASRLARESGINIFITIEGAANEKQYVVEPNFANKAVCRTNGFYSLHVQSWF 465
Db 421 PTDKVEASRLARESGINIFITIEGAANEKQYVVEPNFANKAVCRTNGFYSLHVQSWF 480
Qy 466 GLHKTLOPLVRCVCTDBLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFVTNLTKEF 525
Db 481 GLHKTLOPLVRCVCTDBLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFVTNLTKEF 540
Qy 526 EISPTDRIGAVOYVYEOBLEFDPKYSKSPDILNAIKRVGWSGTSFGAINFALBOL 585
Db 541 EISPTDRIGAVOYVYEOBLEFDPKYSKSPDILNAIKRVGWSGTSFGAINFALBOL 600
Qy 586 FKSKSPNKRKLMILITDGRSYDVRIPMAAHLKGVITYAIGVMAAOEELVIAITHPAR 645
Db 601 FKSKSPNKRKLMILITDGRSYDVRIPMAAHLKGVITYAIGVMAAOEELVIAITHPAR 660
Qy 646 DHSFVDFEFDNLHQVPRRIQNICTEFNSOPRN 678
Db 661 DHSFVDFEFDNLHQVPRRIQNICTEFNSOPRN 693

RESULT 3
Q96DT1_HUMAN PRELIMINARY; PRT; 656 AA.
AC Q96DT1;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Vitrin.
GN Name=VIT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN NCB1;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RA Ren Z.-X., Liu J.G., Mayne R.;
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
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CC -----
EMBL: AF063833; AAL18263.1; -, mRNA.
DR HSSP; 043405; LUBI
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VWA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VMA; 2.
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SEQ SEQUENCE 656 AA; 71768 MW; E242E00DFB07CF2C CRC64;
Query Match 95.5%; Score 3344; DB 2; Length 656;
Best Local Similarity 96.0%; Pred. No. 5.7e-209;
Matches 651; Conservative 1; Mismatches 4; Indels 22; Gaps 1;
Qy 1 MRTVLTAKASVIEMLVLVTGVHNSKETAKKIRKPRFTVPOINCDVAKGIIDPEFV 60
Db 1 MRTVLTAKASVIEMLVLVTGVHNSKETAKKIRKPRFTVPOINCDVAKGIIDPEFV 60
Qy 61 KCPACGDPKHYVTDTDYAASVYCGAAVHSQVLDNSGGKILVRKVAQSGSYKSYNG 120
Db 61 KCPACGDPKHYVTDTDYAASVYCGAAVHSQVLDNSGGKILVRKVAQSGSYKSYNG 120
Qy 121 VOSLSLPRWRESFVLESKPKKGVTPSPALTYSSSSKSPAAGETTKAYQRPPIGTTAAQ 180
Db 121 VOSLSLPRWRESFVLESKPKKGVTPSPALTYSSSSKSPAAGETTKAYQRPPIGTTAAQ 180
Qy 181 PVTLMQLLAVTAAVATPTTLPRPSPAASTTSIPRPOSVGHRSQEMDLMSTATYSSQNR 240
Db 181 PVTLMQLLAVTAAVATPTTLPRPSPAASTTSIPRPOSVGHRSQEMDLMSTATYSSQNR 240
Qy 241 PRADPGIORODPSGAFOKPVGADVSLGLVPEKEELSTOSLEPVSLGDPNCKIDSLFIDG 300
Db 241 PRADP-----GLVPEKEELSTOSLEPVSLGDPNCKIDSLFIDG 278
Qy 301 STSIGKRRFRIOKQLLDVAAQALDIPAGPLMGVVOYGDNPATHFNLKHTNSRDLKTAI 360
Db 279 STSIGKRRFRIOKQLLDVAAQALDIPAGPLMGVVOYGDNPATHFNLKHTNSRDLKTAI 338
Qy 361 EKITORGGLSNVGRASIFVTKNFPSKANGNSGAPNVVVVWDGPTDKVEASRLARES 420
Db 339 EKITORGGLSNVGRASIFVTKNFPSKANGNSGAPNVVVVWDGPTDKVEASRLARES 398
Qy 421 GINIFITIEGAANEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLOPLVRCVCD 480
Db 399 GINIFITIEGAANEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLOPLVRCVCD 458
Qy 481 TDBLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFVTNLTKEFISDPTDRIGAVOYT 540
Db 459 TDBLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFVTNLTKEFISDPTDRIGAVOYT 518
Qy 541 YEORLEFDPKYSKSPDILNAIKRVGWSGTSFGAINFALBOLFKSKSPNKRKLMILI 600
Db 519 YEORLEFDPKYSKSPDILNAIKRVGWSGTSFGAINFALBOLFKSKSPNKRKLMILI 578
Qy 601 TDGRSYDVRIPMAAHLKGVITYAIGVMAAOEELVIAITHPARDSHFVDFEFDNLHQY 660
Db 579 TDGRSYDVRIPMAAHLKGVITYAIGVMAAOEELVIAITHPARDSHFVDFEFDNLHQY 638
Qy 661 VPRRIQNICTEFNSOPRN 678
Db 639 VPRRIQNICTEFNSOPRN 656

RESULT 4
Q3T247_MOUSE PRELIMINARY; PRT; 650 AA.
AC Q3T247;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5;
DE Adult inner ear cDNA, RIKEN full-length enriched library,
DE clone.F930032K14 product:vitrin, full insert sequence.
GN Name=Vlt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=inner ear;
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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Inner ear;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodius R., Shimokawa K.,
 Davis M.J., Wilson L.G., Aldins V., Allen J.E.,
 Amesbury-Imbachao A., Apweiler R., Auraliya R.N., Bailey T.L.,
 Bansal K.P., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 Chiu K.P., Choudhary V., Christofelle A., Clutterbuck D.R.,
 Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 Guernicelli S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 Lium S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 Moutacui-Taber S., Mulder N., Nakano N., Nakanchi H., Ng P.,
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 Okazaki Y., Orlowski V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 Roat B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 Sperling S., Stupka E., Sugita K., Sulana R., Takenaka Y., Taki K.,
 Tammoja K., Tan S.L., Tang S., Taylor M.S., Tenen J., Teichmann S.A.,
 Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeai K.,
 Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hilde W., Bult C.,
 Grimonard S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 Wahlestedt C., Wiatlick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 Fukuda S., Kanamori-Karayama M., Suzuki M., Aoki J., Arikawa T.,
 Iida Y., Imanura K., Itoh M., Kato T., Kawai H., Kawagashita N.,
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 Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 Tagami M., Waki K., Watanabe A., Okamura-Ohno Y., Suzuki H., Kawai J.,
 Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Inner ear;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense transcription in the mammalian transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Inner ear;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nishikido I., Osato N., Saito R., Suzuki H., Yamashita I., Kiyosawa H.,
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 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Giesl C., Godzik A., Gough J.,
 RA Grimonard S., Guernicelli M., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa T., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramchandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yaumishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Inner ear;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iishi Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamashita I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giesl C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bono B.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernicelli S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaeets P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Inner ear;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Inner ear;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Maruwa S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Inner ear;
 RA Arikawa T., Carninci P., Fukuda S., Hashizume M., Hayashida K.,
 RA Hori F., Iida Y., Imanura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Niimiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.


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Db 450 VCDRLRLACSTKCLNSADIGFVIDGSSSVGTSNFRVYQFVANSKEFEISDITDTRVAV 509
Qy 538 QYTEORLEFEGFDKSSKPDILNIAIKRVYWSGGSTGAALNFALEOLFKKSKPKRKLTM 597
Db 510 QYTEQRQFQFDPKISKADILSLAIRVYWSGGSTGAALQYALEOLFKKSKPKRKLTM 569
Qy 598 ILITDGRSYDDVRIIPAMAAHLKGVITTYAIGVMAAOEELVITATHPARHSEFVDFDNL 657
Db 570 IITDGRSYDDVRIIPAMAAHQGVITTYAIGVMAAOEELVITATHPARHSEFVDFDNL 629
Qy 658 HQYVPRITIQNICTEFNSQPRN 678
Db 630 YKIAPRIITQNICTEFNSQPRN 650

RESULT 6
Q95LI2_BOVIN PRELIMINARY; PRT; 652 AA.
ID Q95LI2_BOVIN
AC Q95LI2
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 2.
DT 07-FEB-2006, entry version 16.
DE Vitrin.
GN Name=VIT;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Retina;
RA Ren Z.-X., Liu J.G., Mayne R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial
CC License
DR EMBL; AF063832; AAL18262.2; -, mRNA.
DR HSPB; O43405; IJBI.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PRO0453; VMPADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWF_A; 2.
DR PROSITE; PS50234; VWF_A; 2.
SQ SEQUENCE 652 AA; 70873 MW; 3512421CA6987C51 CRC64;

Query March 80.5%; Score 2818; DB 2; Length 652;
Best Local Similarity 79.8%; Pred. No. 1e-174;
Matches 541; Conservative 49; Mismatches 62; Indels 26; Gaps 2;

Qy 1 MRLVLTLMKASVIMFLVLTGVSNNKETAIKRPFYVPOINCDVAKGIIDPEFIV 60
Db 1 MGIVLTMKASVIMFLVLTGVSNNKETAIKRPFYVPOINCDVAKGIIDPEFIV 60
Qy 61 KCPAGCCDPRHYVGVADYVASSYSCGAHVHSGVLDNSGGKILVRKAVAGSGYKGSYNG 120
Db 61 KCPAGCCDPRHYVGVADYVASSYSCGAHVHSGVLDNSGGKILVRKAVAGSGYKGSYNG 120
Qy 121 VQSIISLPRMRESFVLESKPKKGVITYPSALTYSSSKSPAAGETTKAYORPPIGTTAAQ 180
Db 121 VQSIISLPRMRESFVLESKPKKGVITYPSALTYSSSKSPAAGETTKAYORPPIGTTAAQ 180
Qy 181 PVTLMQLAVALVAVATPTTLPRPSPASATISIRPQSVGHRSQEMDLMTATYTSQNR 240
Db 181 PVTYTAQAPGTTAIAETHHTLPKPSASGTAAGARPOAGRSMKL----- 226
Qy 241 PRADPGIGRQDPSGAARQKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300
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Db 227 --GEP-----AAKMBESVLLDAGFVPEKELSTQSLPEASQGPSCKVDLSFLIDG 274
Qy 301 STSICKRRFRLOKOLADVADVQALDIDGAPGIMGVQYGDNDPATFNKLTNTSRDLTAI 360
Db 275 SSSIGKRRFRLOKOLFIDVQALDIDGAPGIMGVQYGDNDPATFNKLTNTSRDLTAI 334
Qy 361 EKITQRGSLSNVGRALISFVTKNPFSSKANGRSGAPNVVYVMDGWPDTKYEASRLARES 420
Db 335 EKISQRGSLSNVGRALISFVTKNPFSSKANGRSGAPNVVYVMDGWPDTKYEASRLARES 394
Qy 421 GINIFPITIGGAANEQYVVEPANKAVCRNTNGFSLVQSGFGLHKTLOPLVYRQCD 480
Db 395 GVINIFPITIGGASENEQYVVEPANKAVCRNTNGFSLVQSGFGLHKTLOPLVYRQCD 454
Qy 481 TDRLACSKTCLNSADIGFVIDGSSSVGTSNFRVYQFVANSKEFEISDITDTRIGAVQYT 540
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Qy 601 TDGRSYDDVRIIPAMAAHLKGVITTYAIGVMAAOEELVITATHPARHSEFVDFDNLHQY 660
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Qy 661 VPRITIQNICTEFNSQPRN 678
Db 635 VPRITIQNICTEFNSQPRN 652

RESULT 7
Q8K047_MOUSE PRELIMINARY; PRT; 650 AA.
ID Q8K047_MOUSE
AC Q8K047
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Vitrin.
GN Name=Vlt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Eye;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Steplten M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smillie D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Eye;
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Db 330 TAIEKTORGGLSNVGRASISFTTKTFEFGKANGNRCGANVAVWVDGMPDTRKVEEVSRYA 389
Qy 418 RESGNIFFITIEGAENBEKQVYVPEPNFANKAVCTNGNFYSIHHQVSGHKLTOPLVKR 477
Db 390 RESGNIFFITIEGAEREDIHVEPGFASAKVCTNGNFYSFNVSWSLHKTVOPLVKR 449
Qy 478 VCDTRDLRACLSCITCLNSADIGFVIDSSSVGTGNFRTVQFVNTLKEFEISDTRIGAV 537
Db 450 VCDTRDLRACLSCITCLNSADIGFVIDSSSVGTGNFRTVQFVNTLKEFEISDTRIGAV 509
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Qy 658 HQVPRITQICTEFNSOPRN 678
Db 630 YKIPRITQICTEFNSOPRN 650

RESULT 9

Q8BQ41_MOUSE PRELIMINARY: PRT: 628 AA.

AC Q8BQ41_MOUSE integrated into UniProtKB/TrEMBL.

DT 01-MAR-2003, sequence version 1.

DT 07-FEB-2006, entry version 19.

DE 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched

DE library, clone: D130059M21 product: VIRININ homolog.

GN Name: vit;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC NCBI_Taxid=10090;

NCBI_Taxid=10090;

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RA Schonbach C., Sekiguchi K., Sempke C.A., Seno S., Seesa L., Sheng Y.,
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RA Willestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
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RA Iida Y., Imanuma K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
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RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.,
RT "Type transcriptional landscape of the mammalian genome.",
RL Science 309:1559-1563(2005).

[3]

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;

RX PubMed=16141073; DOI=10.1126/science.1112009;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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RA Schirini L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
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RA Datta E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltsev L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontus J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelain A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Willestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wysshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hata A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).

[5]

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Arakawa T., Hara A., Nishikawa Y., Kono H., Adachi J., Ishii Y.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuohi P., Lewis S., Matsuo Y., Nishikawa I., Pesole G., Quackenbush J.,
RA Schirini L.M., Straub F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
RA Blake J., Botelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

[illegible]

| |
|---|
| RESULT 12 |
| ID Q8AW56_BRARE PRELIMINARY; PRT; 553 AA. |
| AC Q8AW56; |
| DT 01-MAR-2003, integrated into UniProtKB/TrEMBL. |
| DT 01-MAR-2003, sequence version 1. |
| DT 07-FEB-2006, entry version 15. |
| DE Novel protein similar to human coagulation factor C homolog (Cochlin, COCH). |
| GN Name=Coch; Synonyms=OTTDARP0000001491; ORFNames=dZ234G15.4-001; |
| OS Brachydanio rerio (zebrafish) (Danio rerio). |
| OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; OC Cyprinidae; Danio. OX NCBI_TaxID=7955; RN [1] RP NUCLEOTIDE SEQUENCE. RA Babbage A.; RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases. CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms CC Distributed under the Creative Commons Attribution-NoDerivs license CC ----- DR EMBL; AL596026; CAD58748.1; -; Genomic_DNA. DR HSSP; O43405; IUBI. DR Ensemble; ENSDARG00000024032; Danio rerio. DR ZFIN; ZDB-GENE-030616-403; coch. DR InterPro; IPR004043; LCCL. DR InterPro; IPR002035; VWF_A. DR Pfam; PF03815; LCCL; 1. DR Pfam; PF00092; VWA; 2. DR PRINTS; PRO0453; VWFADOMAIN. DR SMART; SMO0603; LCCL; 1. DR SMART; SMO0327; VMA; 2. DR PROSITE; PSS0820; LCCL; 1. DR PROSITE; PSS0234; VWFA; 2. SQ SEQUENCE 553 AA; 60351 MW; 4A3B136747C48F0 CRC64; Query Match 33.9%; Score 1187.5; DB 2; Length 553; Best Local Similarity 37.7%; Pred. No. 1.3e-68; |

| Matches | 251, Conservative | 107, Mismatches | 184, Indels | 123, Gaps | 8 |
|---------|---|---|-------------|-----------|---|
| Qy | 16 FLVLVLGVHNS---- | NKETAKKIKRPRKTVQINCDVAAKGIIDPEFIYVKRPGACQDPKY | 71 | | |
| Db | 5 FAVLHVLIGLISLWCTSGSELNVATP----- | ISCGTAAVLSDTHLLVLTPCANCISLWSL | 58 | | |
| Qy | 72 HVGSTDVYASVSYVCAGAAHVSGVDNDSGKILYKVAAGSQYKGSYNGVOSL.SLPRMR | 131 | | | |
| Db | 59 SVFSGSYVYASISSTICGAAIHRGIIGLSCGPVEVHGLQGRTYLYSSAHGVOSQSLSQMSA | 118 | | | |
| Qy | 132 SFIVLESKPKKGVTVPSALTYSSSSKSPAAQAQGETTKAYQRPPIQGTAAQVTLMOQLAVT | 191 | | | |
| Db | 119 SF----- | | 120 | | |
| Qy | 192 VAATPTTLPPRPSAASSTISIPRPOSVGHRSGQEMDLMTATYSSQNRPPADPEIQORD | 251 | | | |
| Db | 121 -TVARTISLPLEVSSQTSSSAIV----- | | 142 | | |
| Qy | 252 PSGAAFOKPVQADVSLGLVPRKEELSTQSLPEVSLGDPNCKIDLSEFLDGSSTIGKRPRRI | 311 | | | |
| Db | 143 ASGAA-KKPVVK-----IVKK----- | PPATAHKDCPVDMLLDSSYNIQGRRTNL | 188 | | |
| Qy | 312 QKQLADVAQALDIPGAPPLMGVVOYGDNPATPHNLKTHTVSRDLKTAIEKITQRGSLSN | 371 | | | |
| Db | 189 QKINVSKLALTKLKTGTQGHVGVQVQTSPTETPELYLNTYTAQVTFALIKIPIYIGAMTN | 248 | | | |
| Qy | 372 VGRAISFVTVKNFESKANGNSGADVVMVVDGMPDKVEBASRLARESGINIFITIEG | 431 | | | |
| Db | 249 TGKAILHTVRNFFSPDFGVRGRYPRVIVFVDDGMPSDVBEAAILARESGINIFEVSAK | 308 | | | |
| Qy | 432 AAENEKQYVVEPNPANKAVCRITNGFSLIHVDSWGLKHTLOPLVKRVCDTDRLCKSTCL | 491 | | | |
| Db | 309 PSPEEASLVSPQDPMRAVCKDNDFETFTPMSWSTYKPFVPLQKCSIDQMCSKTCY | 368 | | | |
| Qy | 492 NSADIGVIVDGSSTVGTFGNFTVLOPFTNLKEPEISPTDRIGAVQYTYEQRLEFGDC | 551 | | | |
| Db | 369 NSVDLGLFLIDSSSVGDNFRLLVDLVSIRASDIDISGRIGAIQCTTYOQRMEFNND | 428 | | | |
| Qy | 552 YSKSPDLINAIKRVGWSGGTSTGAINFALQLFKSKSPKRRKMLIITDGRSYDVRI | 611 | | | |
| Db | 429 HVLKDNMLRALQKIPYMSGGATGDAINFAVRSLPKPRSSNRKFLIITDGOSSYDVVRV | 488 | | | |
| Qy | 612 PAAAAHLKGVITTAIGYMAAAQOELEVIATHPADHSFVDFEFDNLHGYVRRIIONIC-- | 669 | | | |
| Db | 489 PAAAAQREGITVYAVGYAAMPEDLKAWARESPKESHVFETREFTGLGQFOOPIVRGICRD | 548 | | | |
| Qy | 670 -TEEN 673 | | | | |
| Db | 549 FTEEN 553 | | | | |

| | COCH_CHICK | STANDARD; | PRT; | 547 AA. |
|----|--|-----------|------|---------|
| AC | 042163; | | | |
| DT | 30-MAY-2000, integrated into UniProtKB/Swiss-Prot. | | | |
| DT | 01-JAN-1998, sequence version 1. | | | |
| DT | 07-FEB-2006, entry version 39. | | | |
| DE | Cochlin precursor (COCH-5B2). | | | |
| GN | Name=COCH; Synonyms=COCH5B2; | | | |
| OS | Gallus gallus (Chicken). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; | | | |
| OC | Gallus. | | | |
| OX | NCBI_TaxID=9031; | | | |
| RN | [1] | | | |
| RP | NOCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND DEVELOPMENTAL | | | |
| RP | STAGE. | | | |
| RC | STRAIN=White Leghorn; TISSUE=Basilar papilla; | | | |
| RX | MDLID=98409669; PubMed=9736748; DOI=10.1073/pnas.95.19.11400; | | | |
| RA | Heller S., Sheene C.A., Javed Z., Hudspeath A.J.; | | | |
| RT | "Molecular markers for cell types of the inner ear and candidate genes | | | |
| RT | for hearing disorders."; | | | |

```

RL Proc. Natl. Acad. Sci. U.S.A. 95:11400-11405(1998).
CC -1- SUBCELLULAR LOCATION: Secreted protein (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in inner ear structures: the
CC spiral-shaped cells of the basilar papilla. Weaker expression
CC found in the inferior and superior fibrocartilaginous plates and
CC skeletal muscle.
CC -1- DEVELOPMENTAL STAGE: Specifically expressed at the late
CC developmental stages in the cochlea.
CC -1- SIMILARITY: Contains 1 LCCL domain.
CC -1- SIMILARITY: Contains 2 VMFA domains.
CC -1- DATABASE: NAME=Protein SpotLight; NOTE=Issue 4 of November 2000;
CC WWW="http://www.expasy.org/spotlight/back_issues/split004.shtml".
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR HMBP; AF012252; AAC62253.1; -; mRNA.
DR HMBP; O43405; 1JBI.
DR Ensembl; ENSGALG00000009920; Gallus gallus.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR002035; VMF_A.
DR Pfam; PF00815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VMPADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VMFA; 2.
DR GlycoProtein; Repeat; Signal.
KT SIGNAL 1 19 Potential.
FT CHAIN 20 547 Cochlin.
FT FTID=PRO_0000020967.
FT DOMAIN 24 117 LCCL.
FT DOMAIN 162 347 VMFA 1.
FT DOMAIN 364 534 VMFA 2.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
FT DISULFID 30 46 By similarity.
FT DISULFID 50 70 By similarity.
SQ SEQUENCE 547 AA; 59427 MW; 172724242641DF88 CRC64;

Query Match 32.5%; Score 1139; DB 1; Length 547;
Best Local Similarity 37.3%; Pred. No. 1,9e-65;
Matches 229; Conservative 104; Mismatches 165; Indels 116; Gaps 5;

QY 60 VKCPAGQDPRKHYVGTDVVASVSGAAVHSGVLDNCGKILYRKVAGSGVKGSYN 119
DB 44 VLCFANCPMLQFVFGDGIYASLSSVCGAALHGVITNAGAVRVQTLPGGENIPAVHAN 103
QY 120 GVQSLSPRMRESFVLESKPKKGVTPSALTYSKSPAAQAGETTRAYORPIPTTA 179
DB 104 GIGQVLSRMASSFSV-----TPGTNN 125
QY 180 QPTVLKOLLAVTAVVAPFTLPRBPSAASTTSLPRPOSVGHRSGEMDLMSTATYTSQN 239
DB 126 ---LALFVAGRSVATARPAT----- 142
QY 240 RPRADPGLQRDPBGAARQKRVGADVSLGLVPEKELSTQSLPEVSLGDPNCKIDSLID 299
DB 143 -----GKRPKTLERKA-----GNKDKKADIAFLID 168
QY 300 GSTSIGKRRPFIQKOLLADVAQAALDIPAGPLMGVQYGDNPATFNLKHTNSRDLKTA 359
DB 169 GSNYIGQRFFVLQGNFVKAVAMLCIGTEGPHVGVVQASHPKIEFLYKNTAKKEVFA 228
QY 360 IETIQRGSLSNVGRALSFTVKNFPSKANGNSGAPNVVVVVMDPTDKVVEASRLARE 419
DB 229 IKEIGFGGNSNTGKALGHAQKFFSMENRGARKGIPKIIIVFLDGMPSDDLEAGIVARE 288
QY 420 SGNIFFITIGAAENKQYVVEPFAKVCRTNGFSLVQSGFGLHKLQPIYKVC 479
DB 289 FGVAVFIVYVAKPTTEELGMVODIGFDKAVCRNNGSPFSYQMPSPFGTKVKKVLPVQKLC 348
QY 480 DTDRLACSKTCLNSADIGFVIDGSSVGTGNFRFVLQFTNLTKFEISDTDRIGAVQY 539

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DB 349 SHEOMLCKTYNVNIGFLIDGSSSVGESNFRMLLEPISNVAKAFELSDGSKITAVQF 408
QY 540 TYEORLEFGDPKYSKPDILNAIKRVYWGSGTGAIAINPALBQLFKSKPKNRK-LMI 598
DB 409 TYDQRTESFYDYTTKEKVSALNNIRWSGTIGADISTTTNNRFPVYDGNKQNFV 468
QY 599 LITGRSYDVRIPAMAHLKGVITTYAGVMAAELEVIATPHARDSEFFVEFDNLH 658
DB 469 ILTGGQSYDDVRGRAVAQAQKGIIVFSVGVAAPLDDLKMAASERREHFTTFEFTGLE 528
QY 659 QYVPRITQITTEF 672
DB 529 QMVPDVIRGICKDF 542

RESULT 14
COCH_HUMAN STANDARD; PRT; 550 AA.
AC O43405;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 56.
DE COchlin precursor (COCH-582).
GN Name=COCH; Synonyms=COCH582; ORFNames=UNQ257/PRO294;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN NM_117111.1
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Cochlea;
RX MEDLINE=98110569; PubMed=9441737; DOI=10.1101/geno.1997.5067;
RA Robertson N.G., Skvorak A.B., Yin Y., Wernowicz S., Johnson K.R.,
RA Kovatch K.A., Battey J.F., Bieber F.R., Morton C.C.;
RT "Mapping and characterization of a novel cochlear gene in human and in
RL mouse: a positional candidate gene for a deafness disorder, DFNA9.";
RN 121
RN 122
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chan J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Bacon D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandel R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN 131
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ARG-135; ASN-281;
RP SER-353 AND VAL-402.
RA Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
RT "SeattlesNPS, NHLBI HL66682 program for genomic applications, UW-
RT FHRCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN 141
RP N-GLYCOSYLATION, SUBCELLULAR LOCATION, AND PROTEOLYTIC PROCESSING.
RX MEDLINE=2272166; PubMed=12843317; DOI=10.1136/jmg.40.7.479;
RA Robertson N.G., Hamaker S.A., Patriub V., Aster J.C., Morton C.C.;
RT "Subcellular localization, secretion, and post-translational
RT processing of normal cochlin, and of mutants causing the sensorineural
RL deafness and vestibular disorder, DFNA9.";
RL J. Med. Genet. 40:479-486(2003).
RN 151
RP STRUCTURE BY NMR OF 27-126.

```



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Query Match 32.3%; Score 1129.5; DB 1; Length 550;
Best Local Similarity 37.1%; Pred.No.7,8e-65;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7

OY 44 INCNVAGKIIDPEFIVKCPACOPKYNVYGTDDVAASYSGCAVHSGVDLNSGGKIL 103
DB 32 ITCFTRGDIIRKXKADVLCFGCGCPLEEFYVGNIVYASVSSICGAAYVHGVINSNGGPR 91
OY 104 VRKVAQSGYKGSYSYNGVSLPLPMRESFVILESPKPKGVTPYSALTYSSKSPAAQNG 163
DB 92 VYSLPGREYNSVVDANGIQSQMLSHWSASFVYTKGK-----SSTQATNGQA- 137
OY 164 ETTKAYQRRPIGTTAQAQVLTMLQALVYAVATPTTLPRPSPASTTSIRPPQSVGRHS 223
DB 138 -----VSTHAP----- 143
OY 224 QEMDLMTATYTSQGNRPADPGIQRODPSGAFOKPGVADVSLGLVPKEELSTQLEPV 283
DB 144 -----PTGRLLK-----TPKK----- 156
OY 284 SLGDNCKIDSLFLIDGSTISGKRFRRIQKOLLADVAQALDIGPAPPLMGVYQGDNPAT 343
DB 157 -TGKNDCKADI AFLIDGSFNIGQRREPNLQKNFVGKVALMLGIGTBGPHVGLVQASEHPKI 215
OY 344 HFNLTHTNSRDLKTAIEKITRQGLSNVGRALISFTKTFPSKANGNSGAPNVVVYVND 403
DB 216 EYLLKNFTSAKVLPAIKVGRFGNSNGKALKTAQKFFFTVDGVRKGLPKVYVVFID 275
OY 404 GWPDTKVEBASRLARESGINIFITIEGAENEKQYVEPNPANKAVCTNGFYSLHVQS 463
DB 276 GPFSDIDIEBAGIVANEFGVNVIVSAKPIPEELGWODVTVDAVACNNGFSFHYHNP 335
OY 464 WFGHAKTIOLPYKRVCDTDRILACSKTCLNSADIGEVIDGSSSVGTGNFRTVLOFTYNTLK 523
DB 336 WFGTKYKYPFLVQKCTHGNQWCMKTCYVNSVIAFLIDGSSSVGDSNPRMLMEFISNLAK 395
OY 524 EPEISDTDRIGAVOYTYEQRLEFEPDKSSKAPDLIMAIKRVGNSGRTSTAALNFALF 583
DB 396 TFEISDIGAKIAVAOFTYDQRTSFSTSTENYLAIVRNTRVNSGRTATDAISFTVR 455
OY 584 OLFK--KSKPNKRKLMILITDGRSYDDVRIIPMAAHLKGVITYAGVAAQEBLEVAT 641
DB 456 NVFGIRRESPNK-NELVIVTTDQSDTDDVQGPAAHHADGITTFSGVAMAPLDDLKDMWS 514
OY 642 HPARDSFEVDFDNLHQVPRRIIONICTEF 672
DB 515 KPESHAFPTREFTGLEPIVSVINGICRDF 545

RESULT 15
OSEA64 BOVIN PRELIMINARY; PRT; 550 AA.
ID OSEA64 BOVIN PRELIMINARY; PRT; 550 AA.
AC OSEA64
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 6.
DE Coagulation factor C homolog, cochlin.
GN Name=COCH;
OS Bos taurus (Bovine);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Pool;
RC MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RX Smith T.P.L., Grosse W.M., Freyling B.A., Roberts A.J., Stone R.T.,
RA Caasas E., Wray J.E., White J., Cho J., Fehrenking S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McGown C.G.,
RA Petrea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keefe J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA

```

| RT | libraries and construction of a gene index for cattle." | |
|-----------------------|--|--|
| RT | Genome Res. 11:626-630(2001). | |
| RM | (2) | |
| RP | NUCLEOTIDE SEQUENCE. | |
| RC | TISSUE=Poolled; | |
| RA | Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W., | |
| RA | Snelling W.M., Weidman R.T., Smith T.P.L.; | |
| RT | "Sequencing and analysis of Bos taurus full-length insert cDNA | |
| RT | clones." | |
| RL | Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases. | |
| CC | Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms | |
| CC | Distributed under the Creative Commons Attribution-NoDerivs License | |
| CC | ----- | |
| CC | EMBL, BT020705; AAX08722.1; -, mRNA. | |
| DR | SMR, O5E64; 29-124. | |
| DR | Ensembl, ENSBTAG00000021844; Bos taurus. | |
| DR | InterPro, IPR004043; LCCL. | |
| DR | InterPro, IPR002035; VWF_A. | |
| DR | Pfam, PF03815; LCCL, 1. | |
| DR | Pfam, PF00092; VMA; 2. | |
| DR | PRINTS, PR00453; VWFADOMAIN. | |
| DR | SMART, SM00603; LCCL, 1. | |
| DR | SMART, SM00327; VMA; 2. | |
| DR | PROSITE, PS50820; LCCL, 1. | |
| DR | PROSITE, PS50234; VMPA; 2. | |
| DR | SEQUENCE 550 AA; 59594 MW; DB3B21839C68D209 CRC64; | |
| Query Match | 32.1%; Score 1123.5; DB 2; Length 550; | |
| Best Local Similarity | 36.8%; Pred. No. 1,9e-64; | |
| Matches | 232; Conservative 103; Mismatches 177; Indels 119; Gaps 7 | |
| QY | 44 INCDYKAKKIIDPEPIVNCPCAGCDDPKYHYVGTGYVYASYSVCGAAVHSGVLNDSGKIL 103 | |
| DB | 32 ITCSRGRLDIRREKADVLCPGCGCPLEPFSVFCHIIYVASVSI:CGAAVHRVIGHSGGPR 91 | |
| QY | 104 VRKAVGSGYKGSYNGVQSLSLPWRRESFYILESKPKKGVYTPSALTYSSSKSPAAQAG 163 | |
| DB | 92 IYSLPGRNYSVAVANGIQSOLMSHWSAFYTKGK-----SGQEATGQA- 137 | |
| QY | 164 ETKAVGPRPIPGTTAQPVTLMQLLAVVAVPTPTLPSPSAASTSIPRPSQVGHRS 223 | |
| DB | 138 -----VSTHPRAT-----GKR- 148 | |
| QY | 224 QEMDLMTATYTSQGNRPADPGIQRDPGSAFQKPVGADVSLGVPRKEELSTOSLEPV 283 | |
| DB | 149 -----LKKTPPKK----- 156 | |
| QY | 284 SLGDPNCKIIDLFLIDGSTIGKRRFRIOQLLADVQAOLDIGRAPPLMGVVOYGDNPAT 343 | |
| DB | 157 -TGNMDCADIAFLIDGSFNIGORRFNLQKNFVGKVALMLGIGTGGPHGLVQASHPRXI 215 | |
| QY | 344 HPNLKTHTNSDCLKAIEKITORGSLSNVGRALISFTKNFESKANGNRSGANVVVVMVD 403 | |
| DB | 216 EFLYLNFTSADVLPALKEVAFRGNSSTGKLLKHTAQEFPAADGARKGPIPVVVVFID 275 | |
| QY | 404 GMPDQVEAESRLARESGINIFITIEGAANEKQYVPEPNANKAVCTRNGFYSLHVS 463 | |
| DB | 276 GMPSDIDIEAGVAREPVGNNVFIYVAKPIPEBELMGVDVAIVDCAVCANNGEFTSHMN 335 | |
| QY | 464 WFLGHLTIQPIVLRKVCYDTRLACSTKCLNSADIGFVIDGSSSVGTGNFTVLTQFTNLTK 523 | |
| DB | 336 WFGTGYKVPPLQKCTHEOMMCSKTCYNSVIAFLIDGSSSVGSNPFRLMKFVSNIAK 395 | |
| QY | 524 EPEISDPTTRIGAVOYTYEQRLEPEFDKYSKSPDLINAKRGVYSGGTSGTAAINFALE 583 | |
| DB | 396 TFEISDYGAKIAAQQFTYDQRTSESFSTYSTEENVAIIRNTSYNSGGATADALASTYR 455 | |
| QY | 584 QLF--KKSCKPKRKMLITITGRSYDVDRIPAMAHLKGVITYAIGVAAAOEELVIAAT 641 | |
| DB | 456 NVFEGVGRSPRK-NFLVAVTDGQSDVDVDRGPAALAHDAGITTFISGVANAPRDLDKMAAS 514 | |
| QY | 642 HPARDHSFEVDFDNLHQVPRRIIONICTEP 672 | |

Db 515 KPESHAFTRREFTGLEPIVSDVIRGICRDF 545

Search completed: June 7, 2006, 01:19:07
Job time : 307 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 8, 2006, 22:54:30 ; Search time 181 Seconds
(without alignments)
1735.136 Million cell updates/sec

Perfect score: 3502
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Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues
Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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GenCore version 5.1.9
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Run on: June 7, 2006, 01:19:22 ; Search time 52 Seconds
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1141.265 Million cell updates/sec

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ALIGNMENTS

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Sequence 179, Application US/09991181
Patent No. 6913519
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR FILING DATE: 1998-07-09

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVVLTMKASVIEMLVLLVTGVSNKETAKKIKRKFTVPOINCDVAKIIDPEFIY 60
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Db 61 KCPAGCDDPKYHYGVGDVYASYSVCGAAVHSGVLDSGKILVRKAGSGYKGSYNG 120
QY 121 VQSLPLRMRESFVLSEKPKKGVTPSALTYSKSPAAOAGETTKAYORPPIPTTAQ 180
Db 121 VQSLPLRMRESFVLSEKPKKGVTPSALTYSKSPAAOAGETTKAYORPPIPTTAQ 180
QY 181 PVTLMQLLATVVAATPTTLPRSPSAASTTSPRPSVGHRSQEMDLWSTATYSSQNR 240
Db 181 PVTLMQLLATVVAATPTTLPRSPSAASTTSPRPSVGHRSQEMDLWSTATYSSQNR 240
QY 241 PRADPGIQRDDPSGAARQKVGADVSLGLVPKBELSTQSLSEPVSLDPNCKIDLSFLIDG 300
Db 241 PRADPGIQRDDPSGAARQKVGADVSLGLVPKBELSTQSLSEPVSLDPNCKIDLSFLIDG 300
QY 301 STSIGKRFRRIQKQLADVAQALDIGPAGPLMGVGVGDNPAHFNLKHTNSRDLXTAI 360
Db 301 STSIGKRFRRIQKQLADVAQALDIGPAGPLMGVGVGDNPAHFNLKHTNSRDLXTAI 360

Qy 361 EKITORGGLSNVGRALISFVTXKNFPSKANGNRSGAPNVVVWVGWPTDKVEBASRLAES 420
Db 361 EKITORGGLSNVGRALISFVTXKNFPSKANGNRSGAPNVVVWVGWPTDKVEBASRLAES 420
Qy 421 GINIFITIEGAENKQYVVEPNPANKAVCTTNGFYSLHVOSFGLHKTLOPLVKRVD 480
Db 421 GINIFITIEGAENKQYVVEPNPANKAVCTTNGFYSLHVOSFGLHKTLOPLVKRVD 480
Qy 481 TDRLACSTCNSANIGFVIOGSSSVGTGNPFTVLOFTNLTKEREISDTPRIGAVOYT 540
Db 481 TDRLACSTCNSANIGFVIOGSSSVGTGNPFTVLOFTNLTKEREISDTPRIGAVOYT 540
Qy 541 YEORLEFSGFDKXSSKPDILNIAIKRVYWSGGTSTGAINFALBOLFKSKSPKRLMILI 600
Db 541 YEORLEFSGFDKXSSKPDILNIAIKRVYWSGGTSTGAINFALBOLFKSKSPKRLMILI 600
Qy 601 TDGSSYDDVRIPAMAHLKGVITTAIGVMAAOELEVIAITHPADHSEFVDEPNLHOY 660
Db 601 TDGSSYDDVRIPAMAHLKGVITTAIGVMAAOELEVIAITHPADHSEFVDEPNLHOY 660
Qy 661 VPRIIQNICTEFNSOPRN 678
Db 661 VPRIIQNICTEFNSOPRN 678

RESULT 3
US-09-997-333-179
Sequence 179, Application US/09997333
Patent No. 6953836
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C27
CURRENT FILING DATE: US/09/997,333
PRIOR APPLICATION NUMBER: 60/049787
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121 VOSLSLPRMBESFVLESKPKGVTYPSALTSSSKSPAQAQETTKAYORPPIPGTTAQ 180
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181 PVTLMQLAATVAVATPTTLPRPSPASSTTSIPRPOSVGHRSGEMDLMSTATYSSQNR 240
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421 GINIFFTTIGGAENEQYVVERPFANKAVCRITNGFSLVQSMFGHLKLOPLVKRVC 480
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Db 481 TDRLACSKTCNSADIDFVLDGSSVGTGNFRFVLOFVTNLTKFEISDTRIGAVOYT 540
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Db 541 YEORLFEPDKYSSKPDILNAIKRVGYWSGSTGAALNFALEQLFKSKRPNKKMLILI 600
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601 TDGRSYDDVRIIPMAAHLKGVITTYALGVANAAQEELEVIATHPARHDSFVDERDNLHOY 660
Db 601 TDGRSYDDVRIIPMAAHLKGVITTYALGVANAAQEELEVIATHPARHDSFVDERDNLHOY 660
QY 661 VPRILONICTEPNSQPN 678
661 VPRILONICTEPNSQPN 678
Db 661 VPRILONICTEPNSQPN 678

RESULT 4
US-09-992-598-179
Sequence 179 Application US/09992598
Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match      100.0%; Score 3502; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 KCPAGCDDPKYHYVGTGVVYASYSVCGAAVHSGVLNDSGGKIIIVKXVAGOSGYGSVSNQ 120
QY 121 VQSLSPRMRRESFVLESKEPKGVTPYSALTYSKSPAAOAGETTRAYORPPIGTTAAQ 180
DB 121 VQSLSPRMRRESFVLESKEPKGVTPYSALTYSKSPAAOAGETTRAYORPPIGTTAAQ 180
QY 181 PVTLMQLAVTVAVATPTTLPRPSPASATTSIPRPOSVGHRSGEDMLWSTATYTSQNR 240
DB 181 PVTLMQLAVTVAVATPTTLPRPSPASATTSIPRPOSVGHRSGEDMLWSTATYTSQNR 240
QY 241 PRADPGIORDDPSGAFOKGVGADVSLGLVPKBELSTOSLEPVSLGDPNCKIDISFLIDG 300
DB 241 PRADPGIORDDPSGAFOKGVGADVSLGLVPKBELSTOSLEPVSLGDPNCKIDISFLIDG 300
QY 301 STSISGRKRRFIQKQLADVAQALDIGPAGPLMGVVOYGDNPATHFNLKTHNSRDLTAAI 360
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QY 361 EKITORGGLSNVGRASISFTVNIFPSKANGNSGAPNNVVVVWDGMPDTEKVEASRLAES 420
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QY 421 GINIFFITIEGAENREKQYVVEPNPANKAVCRRTGFSLSHQSFGLHKTLOPLVKRYCD 480
DB 421 GINIFFITIEGAENREKQYVVEPNPANKAVCRRTGFSLSHQSFGLHKTLOPLVKRYCD 480
QY 481 TDRLACSKTCNLSADIGFVIDGSSVGTGNRTYLOPVTNLTKPEISDPTDTRIGAVOYT 540
DB 481 TDRLACSKTCNLSADIGFVIDGSSVGTGNRTYLOPVTNLTKPEISDPTDTRIGAVOYT 540
QY 541 YEORLEFGFDKYSKSPDILNAIKRQVYWSGGTSTGAAINFALBOLFKKSKPKRKLMI 600
DB 541 YEORLEFGFDKYSKSPDILNAIKRQVYWSGGTSTGAAINFALBOLFKKSKPKRKLMI 600
QY 601 TDGRSYDDVRIPMAAHLKGVITTAIGVAAAQOELEVIATHPARDHSFVDEPDNLHOY 660
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QY 661 VPRIIIONICTEFPNSOPRN 678
DB 661 VPRIIIONICTEFPNSOPRN 678

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gruney, Austin L.
; APPLICANT: Kljavin, Ivay J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC61
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; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910

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; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 0;
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
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 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 301 STSISGRFRRIQKOLLADVAQALDIGAPGLMGVVOYGDNPATHTNLTHTNSRDLKTAI 360
 361 EKITORGCLSNVGRALISFTKNPFKANGNREGANRVVVVVWDGWPDTDEBASRLARS 420
 361 EKITORGCLSNVGRALISFTKNPFKANGNREGANRVVVVVWDGWPDTDEBASRLARS 420
 421 GINIFPITTEGAENKQYVVEPNFANKAVCTNGEYSLHVSWSGLHKTLOPLVGRVCD 480
 421 GINIFPITTEGAENKQYVVEPNFANKAVCTNGEYSLHVSWSGLHKTLOPLVGRVCD 480
 481 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLQFTVNLTKFEIISDTDRIGAVQYT 540
 481 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLQFTVNLTKFEIISDTDRIGAVQYT 540
 541 YEOBLEFGDKYSKSPDILNAIKRVGYWGGSTGAATFALQULFKSKKPKMKKLMILI 600
 541 YEOBLEFGDKYSKSPDILNAIKRVGYWGGSTGAATFALQULFKSKKPKMKKLMILI 600
 601 TGGRSYDVIRIPAMAAHLKGVITTYAIGVMAAOEELVATHPARDHSFFVDFDNLHGY 660
 601 TGGRSYDVIRIPAMAAHLKGVITTYAIGVMAAOEELVATHPARDHSFFVDFDNLHGY 660
 661 VRIIIONICTEFNSQPRN 678
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RESULT 8
 US-09-989-728-179
 ; Sequence 179, Application US/09989728
 ; Patent No. 7029873
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnayers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C72
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIORITY FILING DATE: 1998-07-02
PRIORITY APPLICATION NUMBER: 60/091978
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/091982
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/092182
PRIORITY FILING DATE: 1998-07-09
Query Match 100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRTVLTMRASVIEMLVLLVLTGVSHNKETAKKIKGPKFTVPQINC DVAKGIIDPEFIY 60
DB 1 MRTVLTMRASVIEMLVLLVLTGVSHNKETAKKIKGPKFTVPQINC DVAKGIIDPEFIY 60
QY 61 KCPAGCQDPKRYHYGTDVYASYSVCGAAHSGVLNDSGKILVRKXAGSGYKGSVNG 120
DB 61 KCPAGCQDPKRYHYGTDVYASYSVCGAAHSGVLNDSGKILVRKXAGSGYKGSVNG 120
QY 121 VOSLSIPRMRESVIESKPKGVTPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
DB 121 VOSLSIPRMRESVIESKPKGVTPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
QY 181 PVTLMQLLATVVAATPTTLPRPSPSAATTSIPRQSVGHRSGQEMDLWSTATYSSQNR 240
DB 181 PVTLMQLLATVVAATPTTLPRPSPSAATTSIPRQSVGHRSGQEMDLWSTATYSSQNR 240
QY 241 PRADPGIQRQDPBGGAARQKRVGADVSLGVPKEELSTQSLPEVSLGDPNCKIDSLFIDG 300
DB 241 PRADPGIQRQDPBGGAARQKRVGADVSLGVPKEELSTQSLPEVSLGDPNCKIDSLFIDG 300
QY 301 STSIGRRFRIRIQQLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAI 360

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|||||
DB 301 STSIGRRFRIRIQQLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAI 360
QY 361 EKITRGGLSNVGRASISFTKNFESKANGNRGAPNVVVWVDGMPDTEVEASRLAES 420
DB 361 EKITRGGLSNVGRASISFTKNFESKANGNRGAPNVVVWVDGMPDTEVEASRLAES 420
QY 421 GINIFITTEGAENKQVVEPNFANKAVCTNGTFYSIAVOSWGLAKTLQPLVRVCD 480
DB 421 GINIFITTEGAENKQVVEPNFANKAVCTNGTFYSIAVOSWGLAKTLQPLVRVCD 480
QY 481 TDLRACSKTCLNSADIGFYIDGSSVGTGNFTYVLOFTVNLTKREBISPTDRIGAVQT 540
DB 481 TDLRACSKTCLNSADIGFYIDGSSVGTGNFTYVLOFTVNLTKREBISPTDRIGAVQT 540
QY 541 YEOBLEFGFDKXSSPDILNAIKRVYSGSTGAIAFALEOLFKSKPNKRKLMI 600
DB 541 YEOBLEFGFDKXSSPDILNAIKRVYSGSTGAIAFALEOLFKSKPNKRKLMI 600
QY 601 TGRSYDVRIRIPAMAHLKGVITTYAIGVMAAQEELVIAITHPADHSFVDFDNLHOY 660
DB 601 TGRSYDVRIRIPAMAHLKGVITTYAIGVMAAQEELVIAITHPADHSFVDFDNLHOY 660
QY 661 VPRIIQICTEFNSQPRN 678
DB 661 VPRIIQICTEFNSQPRN 678

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RESULT 9
US-09-997-349-179
Sequence 179, Application US/09997349
Patent No. 7034106
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavir, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhen
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C37
CURRENT APPLICATION NUMBER: US/09/997,349
CURRENT FILING DATE: 2001-11-15
PRIORITY APPLICATION NUMBER: 60/049787
PRIORITY FILING DATE: 1997-06-16
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/065186
PRIORITY FILING DATE: 1997-11-12
PRIORITY APPLICATION NUMBER: 60/065311
PRIORITY FILING DATE: 1997-11-13
PRIORITY APPLICATION NUMBER: 60/066770
PRIORITY FILING DATE: 1997-11-24
PRIORITY APPLICATION NUMBER: 60/075945

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[illegible]

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MRYVLTWKASVIEFVLVLTGHSNKEATKAKIKRPFTVQINCVDYAKIIPERIV 60
Db      1  MRYVLTWKASVIEFVLVLTGHSNKEATKAKIKRPFTVQINCVDYAKIIPERIV 60

Qy      61  KCPAGCCOPKXHVCTDYVYASVSCGAAVHSGVLNDGGKILVRKVAQSGYKGSYNG 120
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Qy      121  VQSLSPMRRESFVLESKPKKGVTPSALTYSSSKSPAQAGETTKAYORPPIGTTAQ 180
Db      121  VQSLSPMRRESFVLESKPKKGVTPSALTYSSSKSPAQAGETTKAYORPPIGTTAQ 180

Qy      181  PVTLMQLLAVTVAVATPTTLPPSPSAASTSIPRPOSGVHRSQEMDLSTATYSSQNR 240
Db      181  PVTLMQLLAVTVAVATPTTLPPSPSAASTSIPRPOSGVHRSQEMDLSTATYSSQNR 240

Qy      241  PRADGICOROPBSGAFOKPVGADVSLGIVPEELSTOSLEPVSIGDPCKIDLSFLIDG 300
Db      241  PRADGICOROPBSGAFOKPVGADVSLGIVPEELSTOSLEPVSIGDPCKIDLSFLIDG 300

Qy      301  STSICKRRFRIOKOLLADVAQALDIPAGPLMGVVOYGDNPATHTFNLTHTNSRDLKTAI 360
Db      301  STSICKRRFRIOKOLLADVAQALDIPAGPLMGVVOYGDNPATHTFNLTHTNSRDLKTAI 360

Qy      361  EKITORGGISLVNGRAISFVTXNFFSKANGNRSGAGNVVVVMDGMPDKVEBASRLARES 420
Db      361  EKITORGGISLVNGRAISFVTXNFFSKANGNRSGAGNVVVVMDGMPDKVEBASRLARES 420

Qy      421  GINIFITTEGAENEKQYVVEPNANKAVCTNGTFYSIHNOSWGLHKTLOPLVKRYVD 480
Db      421  GINIFITTEGAENEKQYVVEPNANKAVCTNGTFYSIHNOSWGLHKTLOPLVKRYVD 480

Qy      481  TDRLASCKTCLNSADIGFVIDSSVGTGNFRTVLQFVNLTKFEIISDTRIGAVOYT 540
Db      481  TDRLASCKTCLNSADIGFVIDSSVGTGNFRTVLQFVNLTKFEIISDTRIGAVOYT 540

Qy      541  YEORLEFSGDKXSKPDILNAIKRVYWSGGTSTAINFALQOLFKSKSPMKRKLMIILI 600
Db      541  YEORLEFSGDKXSKPDILNAIKRVYWSGGTSTAINFALQOLFKSKSPMKRKLMIILI 600

Qy      601  TDGRSYDVDRIPAMAHLKGVITTAIGVAMAQOELELVATHPADHSEFVDEPNLHOY 660
Db      601  TDGRSYDVDRIPAMAHLKGVITTAIGVAMAQOELELVATHPADHSEFVDEPNLHOY 660

Qy      661  VPRITONICTEFPNSOPRN 678
Db      661  VPRITONICTEFPNSOPRN 678

RESULT 10
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; Sequence 179, Application US/09997653
; Patent No. 7034132
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
```

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; APPLICANT: Deenoyers, Luc
; APPLICANT: Falcon, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerder, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC38
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; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYVLTMKASVTEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVAKGIIDEEFIY 60
DB 1 MRYVLTMKASVTEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVAKGIIDEEFIY 60
QY 61 KCPAGCDDPKYHYVGDVVASYSVCGAAVHSGVLNCGSKILVRVAGSGYKGSYSNG 120
DB 61 KCPAGCDDPKYHYVGDVVASYSVCGAAVHSGVLNCGSKILVRVAGSGYKGSYSNG 120
QY 121 VQSLSLPRWRESFIVLESKRKKGVTYPSALTYSSKSPAAGETTKAYORPIPGTTAQ 180
DB 121 VQSLSLPRWRESFIVLESKRKKGVTYPSALTYSSKSPAAGETTKAYORPIPGTTAQ 180
QY 181 PVTLMQLLAVTVAVATPTTILPRPSPAAGTTSIPRQSVGHRSGEMDLWSTATYTSQNR 240
DB 181 PVTLMQLLAVTVAVATPTTILPRPSPAAGTTSIPRQSVGHRSGEMDLWSTATYTSQNR 240
QY 241 PRADPGIORODPSGAFFQKPVGADVSLGLVPKSELSTQSLPEVSLDPPNCKIDLSFLIDG 300
DB 241 PRADPGIORODPSGAFFQKPVGADVSLGLVPKSELSTQSLPEVSLDPPNCKIDLSFLIDG 300
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QY 301 STSICKRRFRIOKOLLADVAQALDIGPAGPLMGVVOYGDNPATHTENLTKHTNSRDLKTAI 360
DB 301 STSICKRRFRIOKOLLADVAQALDIGPAGPLMGVVOYGDNPATHTENLTKHTNSRDLKTAI 360
QY 361 EKITRGGLSNVGRALISFTTKNPFPSKANKNBSGAPVWVWMDGMPDVBVEASRLARRS 420
DB 361 EKITRGGLSNVGRALISFTTKNPFPSKANKNBSGAPVWVWMDGMPDVBVEASRLARRS 420
QY 421 GINIFPITTEGAENEKOYVVEPNFANKAVCRITNGFSLHVOSWFLGHTLLOPLVKRVD 480
DB 421 GINIFPITTEGAENEKOYVVEPNFANKAVCRITNGFSLHVOSWFLGHTLLOPLVKRVD 480
QY 481 TDRLACSKTCLNSADIGFVIDSSVGTGNFRTVLQFVTNLTKFEISDTRIGAVOYT 540
DB 481 TDRLACSKTCLNSADIGFVIDSSVGTGNFRTVLQFVTNLTKFEISDTRIGAVOYT 540
QY 541 YEQRLEFPGDKSSKRPDLINAIKRVGYWGGTSTGAALNFALEOLFCKSKPKRKLMLI 600
DB 541 YEQRLEFPGDKSSKRPDLINAIKRVGYWGGTSTGAALNFALEOLFCKSKPKRKLMLI 600
QY 601 TDGRSYDVRIPAMAHLKGVTTTVAIGVAMAOEELVATHPARDHSPFVDEPNLHOY 660
DB 601 TDGRSYDVRIPAMAHLKGVTTTVAIGVAMAOEELVATHPARDHSPFVDEPNLHOY 660
QY 661 VPRIIQNICTEFNSOPRN 678
DB 661 VPRIIQNICTEFNSOPRN 678

RESULT 11
US-09-989-293A-179
Sequence 179, Application US/09989293A
Patent No. 7034136

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT FILING DATE: US/09/989, 293A
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR APPLICATION NUMBER: 60/089600
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PRIOR APPLICATION NUMBER: 60/089653
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01

PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTMKASVIMFLVLTGVHSNKEFAKKIKRPFYVPOINCQVAKGIIDPEFIV 60
DB 1 MRTVLTMKASVIMFLVLTGVHSNKEFAKKIKRPFYVPOINCQVAKGIIDPEFIV 60
QY 61 KCPAGCDDPKYHYVGTVDVVASYSVCGAAVHSGVLDSGGKILVRKYAGSGYKGSYNG 120
DB 61 KCPAGCDDPKYHYVGTVDVVASYSVCGAAVHSGVLDSGGKILVRKYAGSGYKGSYNG 120
QY 121 VQSLSPRMRESFVLBSKPKKGYTPSALTYSSSKSPAAQAGETTKAYORPPIPGTTAQ 180
DB 121 VQSLSPRMRESFVLBSKPKKGYTPSALTYSSSKSPAAQAGETTKAYORPPIPGTTAQ 180
QY 181 PVTLMOLLAVTVAVATPTTLPRPSPAASTTISIRPQSVGHRSEMDLMTATYTSSQNR 240
DB 181 PVTLMOLLAVTVAVATPTTLPRPSPAASTTISIRPQSVGHRSEMDLMTATYTSSQNR 240
QY 241 PRADPGIORODPSGAAPKPGADVSLGLVKEELSTQSLPEVLAGPNCIKIDLSFLIDG 300
DB 241 PRADPGIORODPSGAAPKPGADVSLGLVKEELSTQSLPEVLAGPNCIKIDLSFLIDG 300
QY 301 STSIGKRFRIOQLDLADVAQALDIGPAGPLMGVVOYGDNPATFNLKTHNSRDLKTAI 360
DB 301 STSIGKRFRIOQLDLADVAQALDIGPAGPLMGVVOYGDNPATFNLKTHNSRDLKTAI 360
QY 361 EKITQGGLSNVGAISFTYTNKFSKANGNRSGAPNVVVWVDMQPDYKVEABRLARES 420
DB 361 EKITQGGLSNVGAISFTYTNKFSKANGNRSGAPNVVVWVDMQPDYKVEABRLARES 420
QY 421 GINIFITIEGAANEQYVVEPNFANKAVCRTGTFYSLHVQSPFGLAKTLQPLVKRYCD 480
DB 421 GINIFITIEGAANEQYVVEPNFANKAVCRTGTFYSLHVQSPFGLAKTLQPLVKRYCD 480
QY 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRIVLQFVTNLTKFEISDTRIGAVQYT 540
DB 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRIVLQFVTNLTKFEISDTRIGAVQYT 540
QY 541 YEORLEFGFDYSSKRPDIINAIKRVGWSGTSFGAAINFLAEOLFKKSPNKKMILI 600
DB 541 YEORLEFGFDYSSKRPDIINAIKRVGWSGTSFGAAINFLAEOLFKKSPNKKMILI 600
QY 601 TDGRSYDDVRIPAAAHKGVITAYAGVAAQOELEVIATHPARDHSFVDEDFNLHOY 660
DB 601 TDGRSYDDVRIPAAAHKGVITAYAGVAAQOELEVIATHPARDHSFVDEDFNLHOY 660
QY 661 VPRIIIONICTEFNSQPRN 678
DB 661 VPRIIIONICTEFNSQPRN 678

RESULT 12
US-09-907-794A-227
Sequence 227, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi


```

: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/905.125A
: CURRENT FILING DATE: 2001-07-12
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
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: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
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: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 227
: LENGTH: 550
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-905-125A-227

Query Match      32.3%; Score 1129.5; DB 2; Length 550;
Best Local Similarity 37.1%; Pred. No. 9.5e-97;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

QY 44 INCVKAGKIIDPEFIYKCPAGCDDPKHVVGTDVVYSSVCGAAYHSGVLDSGKIL 103
DB 32 ITCTRGADIRKEKADYVCPGCGPLEESVYGNIVYASVSSICGAAYHGVISNSGGEVR 91
QY 104 VRKVGOSGYKGSYNGVOSLSLPRWRESFVLESKPKGVYTSALTYSSSKSPAQAQ 163
DB 92 VYSLPGKENTSSVDANGOSQMLSRMSASFVTKG-----SSTQENATGA- 137
QY 164 ETKAYORPPIPGTTAOPVTLMLLAVTVAATPTTLPRSPSAASTTSIRPOSVGHRS 223
DB 138 -----VSTAHF----- 143
QY 224 QEMDLMTATYTSQNRPRADPGIORODPSGAFOKPYGADVSLGVKPELSTQSLPEV 283
DB 144 -----PTGKRLKK-----TPKK----- 156
QY 284 SLGDPNCKIDLSFLIDSTSGIKRRFRIOQLADVAQALDIDGPAPLMGVVOYGDNPAT 343
DB 157 -TGKDKCADIAFLIDGSFNIGRRFNLQKNFVGKVALMLGIGTEGPHVGLVQASSEHKI 215
QY 344 HFNLTHTNSHDLKTAIEKLTORGGLSNVGAISFVTNKFPSKANGNBSGAPNVVVVMD 403
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DB 216 EFLYKNFTSADVYFAIKEVGFRRGNSNTGALKHTAQKEFTVDAGVRKGI PKVVVFID 275
QY 404 GMPFDKYEBSRLARESGINIFITIEGALENEKQYVVEPFAKAVCRTNGFSLVQS 463
DB 276 GMPSDDIIEAGIVAREGVANFVSVAKPIPEELGMVQDVTVDKAVCRNNGFFSYMPN 335
QY 464 WFLGHTLOPLVKECDTDLRACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFPTNLTK 523
DB 336 WFGTTKTVKPLVQGLCTHEQWMSKTCYNSVNI AFLIDGSSSVGDSNFRILMEFVSNIAK 395
QY 524 EPEISDPTDRIGAVQYTYEQRLPEFGPKYSKPIILAIKRVGYSGCTSTGAINFAL 583
DB 396 TFEISDGAIKAAVQFYDQRTFESSFYDSTKEVLAVINIRIYMSGTATGDAISFTVR 455
QY 584 QLFK--KSKPKRKLMLITDGRSDVRI PAMAAHLKGVITYAIGVMAAOELEVIAT 641
DB 456 NVFGPIRESFVK-NFLVIYTDGQSYDVQGPAAAHAGITITRISVGVAAPLDLKOMAS 514
QY 642 HPARDHSFVDEFDNLHQYVPRITQNICTEF 672
DB 515 KPRESHAFTRFETGLEPIVSDVIRGICRDF 545

RESULT 14
US-09-902-775A-227
Sequence 227, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Deenoyers, Luc
: APPLICANT: Bacon, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvarolef, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/902.775A
: CURRENT FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: PCT/US99/20594
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: PRIOR APPLICATION NUMBER: PCT/US99/20944
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: PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 227
LENGTH: 550
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-227

Query Match 32.3%; Score 1129.5; DB 2; Length 550;

Best Local Similarity 37.1%; Pred. No. 9.5e-97;

Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

44 INCVKAGKIDPEITVCPAGCOPKHYVGTVDYASVSSVCGAASVGLDNGGKIL 103
32 ITCTRGIDIRKXADVLCPGCCPEBSVGNIVYASVSTCGAARGVINSGGFVR 91
104 VRKVASGSGYKSGSYNGVQSLSPRMRESFVLESKPKGVYPSALTYSSSKPAAQ 163
92 VYSLPGRNYSVDANGIQSQMLSRWSASFVTKGK-----SSTQKATGQA- 137
164 ETTAKYQRPPIPTTAQVITLMQLAVYVAATPTTLRPSBSAASTISIRPQSVGRS 223
138 -----VSTAH----- 143
224 QEMDLSTATYTSSQNRPRADPGIQRDPGSAFGKPVGADVSLGLVKEELSTQSLBPV 283
144 -----PTGKRKK-----TPEKK----- 156
284 SLGDPNCKIDSLFLIDGSTSGKRFRIOKOLLADVAQALDIGAPGLMGVQYGNPAT 343
157 -TGKKDCADIAFLIDGSFNIGORFNLQKNFVKVALLMIGTSGPHVGLVQASHPKI 215
344 HFNILKTHNSRDLTALEKITQRGSLSVGRALSFVTYKNFSKANGNSGAPNVVYVND 403
216 EFYKKNFTSADVFAIKEVGRGNSNTGKALKTAQKFFVVDAGVAKGIPKVVVVID 275
404 GMPDKVEEARLARESGINIFETIEGAENEKQYVVEPNPANKAVORTGFSYLAHQS 463
276 GMPSDDLAEAGIVAEFGVNVFIVSAKPIBELAMVDVTFVDVAKRNGFFSYHPNP 335
464 WFGJHKTLOPLVKKVCDTRDLACSKTCLNSADIGFVIDSSSVGTGNFRVLFQVYNLT 523
336 WFGTKTVKPLVQKLTCHGOMMCSKTCTYNSVNIAPLIDGSSVSGNSRMLMEFNSIAK 395
524 EFEISDTRIGAVOYTYEQRLERGFEDKYSKPDILNAIKAVGYWGGSTGGAINEALE 583
396 TFEISDIGAKIAAOFYTDORTEFSTYSTEENLAVIRNIRYNSGGTATGDAISFTVR 455
584 QLPK--KSKPKRKMLITDGRSYDVRIPAMAAHLKGVITTAIVGMAAQEELVAT 641
456 NVFGPIRSPPK-NFLVITVTDGQSDVDVQGPAAAHADGITTFVGVAMAPLDLKDMS 514
642 HPARDHSFVDEFDNLHQYVPRIIQNICTEF 672

Db 515 KPESHAFRTREFTGLEPIVSDVIRGLCRDF 545
RESULT 15
US-09-906-700-227
Sequence 227, Application US/09906700
Patent No. 6723535
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Par, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 1046-14
CURRENT APPLICATION NUMBER: US/09/906,700
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-700-227

Query Match 32.3%; Score 1129.5; DB 2; Length 550;
Best Local Similarity 37.1%; Pred. No. 9.5e-97;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

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QY      44 INCVYKAKKIIDPEFIYKCPAGCCODPKYHYVGTVDYASYSVCGAAVHSGVLDSNGGKIL 103
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      32 ITCFTRGIDIRKEKADVLCPGGCCPLEEFSYGNIVYASVSSICGAAVHGVISNGGPRV 91
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     104 VRKYAGSGYKGSYNGVQSLSPRMRESFIYLESGPKKGYTPSEALTYSSSKSPAAQAG 163
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      92 VYSLPGRENYSVDANGIQSOMLSHMSASFVYTKGK-----SSTQENTGQA- 137
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     164 ETTKAYORPPIPGTYAOPVTLMOLLAVTVAVATPTTLPRPSPSASTTSIPRQSVGHR 223
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     138 -----VSTAHF----- 143
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     224 QEMDLNSTATYTSSQNRPRADPGIORQDPSCGAAPKYGADVSLGLVPKEELSTOSLEPV 283
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     144 -----PTGKRLLK-----TPKK----- 156
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     284 SLGDPNCKIDSLPIDGSTSGKRRFRIOQLADVAQALDIPAPLPMGVQYGDNPAT 343
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     157 -TGKDCADKADIAFLIDGSFNIGORRPNQKNFVGKVALMLGITEGPHVGLVQASEHPXI 215
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     344 HFNILKTHNSRDLTAIEKITORGGLSNVGRASIFVTNPFPSKANGNSGAPNVVYVMD 403
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     216 EFYLNFTSAKDVLFAIKEVGFRRGNSNTGKALKHTAQKFTVDAGVRKGIPIKVVVVFID 275
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     404 GMPFDKYEBSRLARESGINIFITIEGAENEEKYVEBPANKAVCRTNGFYSLHQ 463
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     276 GMPSDDIEEAGIVAREGVNFIIVAKPIPEELGAVODVTFVDAVCRNNGFPSYHMPN 335
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     464 WFGLAHTLQPLVKKVCDTRLACSKTCUNSAADIGFVIDSSSVGTGNFRVLOEVTNLT 523
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     336 WFGTTKYVKPLVQKLTCHQCMCKTCYNSVNIAPFLIDSSSVGDSNFRMLLEFVSNIAK 395
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     524 EFEISDTDTIRIGAVQYTYEQRLEFGPKYSKPDILNAIKRVGWSGGTSGAINEPALE 583
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     396 TFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVIRNIRYWSGGTATGDAISFTVR 455
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     584 QLEK--KSKPNKRKLMILITDGRSYDDYRIPAMAAHLKGVTYTAIGVWMAAQBELVIAT 641
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     456 NVFGPIRESPNK-NFLVIVTDGQSYDVQGPAAAAHAGITTFVGVAMAPLDLDKDMAS 514
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     642 HPARDHSFVDEFDNLHQYVPRITICTEF 672
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     515 KPKEASHAFTRFTGLEPIVSDVIRGICRDF 545
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: June 7, 2006, 01:20:53
Job time : 55 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2006, 01:14:17 ; Search time 44 Seconds
(without alignments)
1482.613 Million cell updates/sec

Title: US-10-063-540-34

Perfect score: 3502

Sequence: 1 MRLTVLTMKASVIEMLPLV.....QYVPRITQICTEFNSQPRN 678

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_80:.*
2: PIR1:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|---------------|--------------------|
| 1 | 554 | 15.8 | 3124 2 A40020 | collagen alpha 1(X |
| 2 | 504.5 | 14.4 | 3137 2 A37797 | collagen alpha 3(V |
| 3 | 501.5 | 14.3 | 496 2 A37979 | cartilage matrix P |
| 4 | 490 | 14.0 | 493 2 A33809 | cartilage matrix P |
| 5 | 490 | 14.0 | 500 2 S6522 | cartilage matrix P |
| 6 | 471.5 | 13.5 | 3176 2 CGH03A | collagen alpha 3(V |
| 7 | 331 | 9.5 | 1857 2 S31212 | collagen alpha 1(X |
| 8 | 331 | 9.5 | 1888 2 S78476 | collagen alpha 1(X |
| 9 | 329.5 | 9.4 | 1747 2 A54849 | collagen alpha 1(V |
| 10 | 329.5 | 9.4 | 1747 2 A45974 | collagen alpha 1(X |
| 11 | 314.5 | 9.0 | 567 2 T28797 | hypothetical prote |
| 12 | 298 | 8.5 | 741 2 T46488 | hypothetical prote |
| 13 | 280.5 | 8.0 | 929 2 S1037 | type XII collagen |
| 14 | 279 | 8.0 | 3051 2 S42373 | hypothetical prote |
| 15 | 266 | 7.6 | 2813 1 VMU | hypothetical prote |
| 16 | 262.5 | 7.5 | 843 1 A40970 | undulin 1 - human |
| 17 | 252.5 | 7.2 | 1019 1 A32856 | collagen alpha 1(V |
| 18 | 231 | 6.6 | 1153 1 RWH03B | cell surface glyco |
| 19 | 229 | 6.5 | 550 2 T23760 | hypothetical prote |
| 20 | 229 | 6.5 | 1153 2 S00551 | leukocyte surface |
| 21 | 228 | 6.5 | 1163 1 RWH03C | cell surface glyco |
| 22 | 226.5 | 6.5 | 427 2 G00039 | von Willebrand fac |
| 23 | 216.5 | 6.5 | 1025 2 S34839 | collagen alpha 1(V |
| 24 | 213.5 | 6.1 | 414 2 S00323 | von Willebrand fac |
| 25 | 213.5 | 6.1 | 1286 2 T18397 | protein MO1E0.2 I |
| 26 | 210.5 | 6.0 | 2098 2 T18397 | protein CTRP - mal |
| 27 | 209.5 | 6.0 | 1022 2 S04111 | collagen alpha 2(V |
| 28 | 209 | 6.0 | 918 2 S23377 | collagen alpha 2(V |
| 29 | 205 | 5.9 | 1028 1 CGH03A | collagen alpha 1(V |

| | | | | |
|----|-------|-----|----------------|--------------------|
| 30 | 205 | 5.9 | 1029 1 S21369 | collagen alpha 2(V |
| 31 | 204 | 5.8 | 11055 2 T16580 | hypothetical prote |
| 32 | 203.5 | 5.8 | 1170 2 S03308 | cell surface glyco |
| 33 | 203.5 | 5.8 | 1180 2 A35854 | integrin alpha-1 c |
| 34 | 200 | 5.7 | 238 2 C35243 | collagen alpha 2(V |
| 35 | 200 | 5.7 | 917 2 S09646 | collagen alpha 2(V |
| 36 | 200 | 5.7 | 1018 1 CGH02A | collagen alpha 2(V |
| 37 | 195 | 5.6 | 1163 2 A55226 | lymphocyte functio |
| 38 | 193 | 5.5 | 1151 2 A55348 | integrin alpha-1 c |
| 39 | 188.5 | 5.4 | 272 2 A55348 | integrin alpha-1 c |
| 40 | 187.5 | 5.4 | 1170 2 T15914 | integrin alpha 2 s |
| 41 | 184.5 | 5.3 | 643 2 T19549 | hypothetical prote |
| 42 | 182.5 | 5.2 | 1181 2 A33998 | integrin alpha-2 c |
| 43 | 178 | 5.1 | 763 2 I50807 | complement factor |
| 44 | 171 | 4.9 | 712 2 A45638 | immunodominant mic |
| 45 | 170.5 | 4.9 | 1178 2 S44142 | VLA-2 protein homo |

ALIGNMENTS

RESULT 1
A40020
collagen alpha 1(XII) chain precursor - chicken
N:Alternate names: fibrochimerin
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C:Accession: A40020; A34485; B34485; A28037; S23814; S22524; S28811
R:Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shimomura, T.; Tanaka, H.; Nishida, Y.; Obar
J. Cell Biol. 115, 209-221, 1991
A:Title: The complete primary structure of type XII collagen shows a chimeric molecule w
nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
A:Reference number: A40020; MUID:92011862; PMID:1918137
A:Accession: A40020
A:Molecule type: mRNA
A:Residues: 1-3124 <YAM>
A:Cross-references: UNIPARC:UPI0000126D2D; GB:D00824; NID:922810; PIDN:
C:Species: Gallus gallus (chicken)
A:Note: In the authors' translation residues 1216-1219 are shown after residue 1235 and,
R:Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Reest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A:Title: Type XII collagen. A large multidomain molecule with partial homology to type I
A:Reference number: A34485; MUID:9062079; PMID:2584192
A:Accession: A34485
A:Molecule type: mRNA
A:Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>
A:Cross-references: UNIPARC:UPI0000171233; EMBL:J05137; NID:9211284; PIDN:AAA48635.1; PI
A:Accession: B34485
A:Molecule type: protein
A:Residues: 2772-2792; 2846-2873 <GOR2>
A:Cross-references: UNIPARC:UPI0000173C3F; UNIPARC:UPI0000173C40
R:Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A:Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA c
A:Reference number: A28037; MUID:87317590; PMID:3476925
A:Accession: A28037
A:Molecule type: mRNA
A:Residues: 2960-2976, 'F', 2978-3074, 'AG', <GOR3>
A:Cross-references: UNIPARC:UPI0000171234; EMBL:M17375; NID:9211649; PIDN:AAA48718.1; PI
A:Note: this sequence has been revised in reference A34485
R:Koch, M.; Bernasconi, C.; Chiquet, M.
Eur. J. Biochem. 207, 847-856, 1992
A:Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of
A:Reference number: S23814; MUID:9236621; PMID:1333460
A:Accession: S23814
A:Molecule type: protein
A:Residues: 'X', 1333, 'Q', 1335-1347, 1914-1928, 2504, 'X', 2506, 'X', 2508-2511, 'X', 2513-2517 <
A:Cross-references: UNIPARC:UPI0000173C41; UNIPARC:UPI0000173C42; UNIPARC:UPI0000173C43
R:Dublet, B.; van der Reest, M.
J. Biol. Chem. 262, 17724-17727, 1987
A:Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-
A:Reference number: S22254; MUID:88087065; PMID:3121603
A:Accession: S22254
A:Molecule type: protein

QY 451 CERNNGF-----YSLHVSQMFGL----- 467
Db 356 STSQITGRVQGITPMIAGKQHVLSVGPOTTALANVDLSPTDTEYQIVNVMKGLITPSEPI 415
QY 468 --HKTLPVYKRVCDTDLRACSKTCLNSADIGFVIDSSSVGTGNFRYLVQFVNLTK 524
Db 416 TIMEKTQGVK-----QVECSRGVDVADAVFLVDGSSIGIANVVKRAFLIEVLVKS 468
QY 525 FEISTDTRIGAVQVTEEDRLFEFGPKYSKSPDILNAIKRWGVSGSTSGAANFPLEQ 584
Db 469 FEISPRKQVQISLVQYSRDPHMEPSLNKYNKVDIQLQINTFPYRGSTNGKATTYREK 528
QY 585 LF---KKSQPNKRKMLMITTDRSYDDVRIPAMAHLKGVITYAIGVMAAOEELEVIAT 641
Db 529 VFTVTSKGRSPNPRVWMLITDQKSSDAFKEPATKADADVEIFAVGVKDAVRELEAIAS 586
QY 642 HPARDHSFFVDEFDNLHQYVPRRIQNICTEFNQ 675
Db 589 PPAETHVYTVEDFDFAFORISFELTOSVCLRIE 622

RESULT 2

A37797
collagen alpha 3(VI) chain precursor - chicken
C1:Species: Gallus gallus (chicken)
C1:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext_change 16-Aug-2004
C1:Accession: A37797; A34270; A32674
R1:Doliana, R.; Bonaldo, P.; Colombatti, A.
J. Cell Biol. 111, 2197-2205, 1990
A1>Title: Multiple forms of chicken alpha3(VI) collagen chain generated by alternative splicing
A1:Reference number: A37797; MUID:91035630; PMID:197751
A1:Accession: A37797
A1:Molecule type: mRNA
A1:Residues: 1-253;312-321;434-453;504-518;635-655;704-717;832-853 <DOL>
A1:Cross-references: UNIPROT: P15989; UNIPARC:UPI0000173C31; UNIPARC:UPI0000173C32; UNIPARC:UPI0000173C33; UNIPARC:UPI0000173C34; UNIPARC:UPI0000173C35
R1:Bonaldo, P.; Russo, V.; Buccicci, F.; Doliana, R.; Colombatti, A.
Biochemistry 29, 1245-1254, 1990
A1>Title: Structural and functional features of the alpha3 chain indicate a bridging role in the triple helix of type I collagen
A1:Reference number: A34270; MUID:90212613; PMID:2322559
A1:Accession: A34270
A1:Molecule type: mRNA
A1:Residues: 224-2871 <BON>
A1:Cross-references: UNIPARC:UPI0000173C38; GB:M24282
A1:Note: The authors translated the codon TTC for residue 1916 as Leu and TTC for residue 1917 as Phe
R1:Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 264, 20235-20239, 1989
A1>Title: The carboxyl terminus of the chicken alpha3 chain of collagen VI is a unique motif
A1:Reference number: A32674; MUID:90062147; PMID:2584214
A1:Accession: A32674
A1:Molecule type: mRNA
A1:Residues: 2151-2199;2792-3137 <BO2>
A1:Cross-references: UNIPARC:UPI0000173C39; UNIPARC:UPI0000173C3A; GB:M24282
C1:Genetics:
A1:Insertions: 30/1; 236/1; 437/1; 638/1; 838/1
C1:Superfamily: collagen VI
C1:Keywords: alternative splicing; cell binding; coiled coil; connective tissue; extracellular matrix
F1:1-25/Domain: signal sequence #status predicted <SIG>
F1:26-3137/Product: collagen alpha 3(VI) chain #status predicted <MAT>
F1:26-2042/Domain: non-collagenous #status predicted <NNC>
F1:36-202/Domain: von Willebrand factor type A repeat homology <VM01>
F1:239-404/Domain: von Willebrand factor type A repeat homology <VM02>
F1:442-607/Domain: von Willebrand factor type A repeat homology <VM03>
F1:642-807/Domain: von Willebrand factor type A repeat homology <VM04>
F1:840-1004/Domain: von Willebrand factor type A repeat homology <VM05>
F1:1033-1197/Domain: von Willebrand factor type A repeat homology <VM06>
F1:1237-1400/Domain: von Willebrand factor type A repeat homology <VM07>
F1:1439-1604/Domain: von Willebrand factor type A repeat homology <VM08>
F1:1639-1804/Domain: von Willebrand factor type A repeat homology <VM09>
F1:1838-2010/Domain: von Willebrand factor type A repeat homology <VM10>
F1:2043-2378/Domain: collagenous #status predicted <COL>
F1:2045-2047/Region: cell attachment (R-G-D) motif
F1:2153-2155/Region: cell attachment (R-G-D) motif

F:2159-2161/Region: cell attachment (R-G-D) motif
F:2379-2137/Domain: non-collagenous #status predicted <CNC>
F:2405-2577/Domain: von Willebrand factor type A repeat homology <W11>
F:2623-2806/Domain: von Willebrand factor type A repeat homology <W12>
F:2803-2846/Domain: platelet glycoprotein Ib-like #status predicted <GPI>
F:2954-3039/Domain: fibronectin type III repeat homology <FN3>
F:3072-3122/Domain: animal knittiz-type proteinase inhibitor <BRI>
F:201,2084,2436,2563,2581,2633,2867,2920,3003/Binding site: carbohydrate (asn)
(covalent

Query Match 14.4% Score 504.5; DB 2; Length 3137;
Best Local Similarity 30.7%; Pred. No. 8.9e-25;
Matches 121; Conservative 87; Mismatches 155; Indels 31; Gaps 8;

OY 293 DLSFLIDSTSIKKRRFIQKOLADVAQALDIPAGLGMVVOYGNDPAHFNLKHTN 352
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Db 38 DIIFLVDSWSISIGKEHFOVLVEFLDYVKALDVCGNDPRFALVDFSGNPHTFOLTYPSS 97
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
OY 353 SRDKTALTEKTQRGSLNVNGRAISFYTKNFPSKANGRS--GAPNVVMVWDGPMDKY 410
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 98 NODVLSIANNPWPWGSGSKTGKGLTYLTENHLTKRASGEVPQIVITVLDGOSDDV 157
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
OY 411 EASRLAESGINIFTITEGAENEKOYVEPFANAVCRGTGFYSIAVOSFGHKTT 470
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 158 ALPSSVLKSAHYNMIAVGQDAVEGELKEIASRPDT-----HLFNIENFTALHG I 208
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
OY 471 LQPLVK-RVCDDTLRLACKS-----TCLNSADIGFVIDGSSSVGTGNFRVLOPTNLT 522
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 209 VGDVLVASVRTMTPEQAQAKGLVKDITAQESADILFLIDGSNDIGSVVFQAIRFLVNL I 268
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
OY 523 KEFELSDDTRTIGAVQYYVEORLEFERGPDYKSKSDIINAIKRGVWSG-GRSTGA INFA 581
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 269 ESLRVGAQQIHIGVAYVSDQPRTEPALNSYSTKADVLDVAHALSPRGKEANTAALEYV 328
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
OY 582 LEOLFPKSKPMK-----RKMLILTDCRSYDVDPAPMAAHLKVITYTAIGVAAAQBEL 636
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 329 VENLFQTQAGSRIEEAVQGIIVLISGGESSDDIRBGLLA VKQASIFRSISGLNAADAHEL 388
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OY 637 EVIATHPARDHSFFVDEFD--NLHQVVRITIQNT 668
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Db 389 QQIAT---DGSFAFTALDIRNLALRELLLPNI 418
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:

RESULT 3
A37979 cartilage matrix protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004
A:Accession: A37979; B37979
R:Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Shi
U. Biol. Chem. 265, 19624-19631, 1990
A>Title: Structure and chromosomal location of the human gene encoding cartilage matrix
A:Reference number: A37979; MUID:91060568; PMID:2246248
A:Accession: A37979
A:Molecule type: DNA
A:Residues: 1-496 <JEN>
A:Cross-references: UNIPROT:P21941; UNIPARC:UPI000004FLIED; GB:J05667
A:Accession: B37979
A:Molecule type: mRNA
A:Residues: 157-290 'L' 292-496 <JE2>
A:Cross-references: UNIPARC:UPI000016AE68; GB:M55683; GB:J05666; GB:J05667; MID:91806511
C:Genetics:
A:Gene: GDB:CRM
A:Cross-references: GDB:127280; OMIM:115437
A:Map position: 1p35-1p35
A:Insertions: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C:Complex: homotrimer
C:Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
C:Keywords: glycoprotein; homotrimer
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-496/Product: cartilage matrix protein #status predicted <MAT>
F:339-206/Domain: von Willebrand factor type A repeat homology <VWA1>
F:227-262/Domain: EGF homology <EGF>
F:273-437/Domain: von Willebrand factor type A repeat homology <VWA2>

F:726.344/Binding site: carbonylhydride (Asn) (covelent) #status predicted
F:1221-238,224-247,249-262/Disulfide bonds: #status predicted

Query Match 14.3%; Score 501.5; DB 2; Length 496;
Best Local Similarity 28.8%; Pred. No. 8,9e-26;
Matches 129; Conservative 80; Mismatches 178; Indels 61; Gaps 9;

QY 273 EELSTQSLIEPVSLGPNCK---IDLSFLIDGSTSIGKRPRRIQKQLADVAQALDIDIPAG 329
DB 19 QALCSGPGIAPSRGRH-LCTRPTPLDVFVVDSSKSVPRVEFEKKYVFLSQYIESLDVGNPA 77
QY 330 PLMGVVOYGDNDPATEFNLKTHNTSRDLKTAIEKITQRGGLSNVGRALSFWTKNFSKANG 389
DB 78 TRVGNNVNASYTKQSESLAAHYSKALLQAVRIQLPLSTGTMTGLAIFATKAFGBAG 137
QY 390 NRGAPN---VVVMVDGMPDTKVEBASRLARESGINIFITTEGAENE--KQYVVEPN 444
DB 138 GRSRSPDISKVIIVTDGRPODSVOPDSARARASGVLEFAIGV-GSDVKATLRLRIASEPQ 196
QY 445 FANKAVCRNRYGYSLSHVOSFGLHKTLP-----LVKRCQDRLALCASTCLNS----- 493
DB 197 DEHVD-----YVESIVYEKLSRFOEAFCVSDICATGDHDCEDQCISSPSSTY 246
QY 494 -----ADIGFVIDSSSVGTGNFRTVLQFVNTLTKEFE 526
DB 247 CACHGFTLNSDQKTCNVSGSGGSSATDLVFLIDGSKSVREPNFELVKKFIISQIVDTLD 306
QY 527 ISDITDRIGAVOYTTTEQRLEFEGDKYSKRPDIINAIRGYMSGGISTGAINFALQELF 586
DB 307 VSDKLAQVGLVOYSSSVROEFPILGRFHTKDKDKAARNMSYMEKGMTGALXYLI DNSF 366
QY 587 KKS---KPKRKLTMLITDGRSYDVRIPAMAAHLGVITTYAIGVMAAOEELVITATP 643
DB 367 TVSSGARPEAQKVGIVFTDGRSODYINDAKKAKADLGFPMKFAVGVADELRILASEP 426
QY 644 ARDHSFVDEPDNLHQYVERIIONICTE 671
DB 427 VAEHFYTADFTKINQIGKKIKICVE 454

RESULT 4
A33809
cartilage matrix protein precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33809; A26354
R:Kliss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimberger, E.; Argy
J. Biol. Chem. 264, 8126-8134, 1989
A:Title: Structure of the gene for cartilage matrix protein, a modular protein of the ex
trins, Von Willebrand factor, complement factors B and C2, and epidermal growth factor.
A:Reference number: A33809; MUID:89255246; PMID:2542265
A:Accession: A33809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <K15>
A:Cross-references: UNIPROT:P05099; UNIPARC:UPI000004F1EF; GB:X12346; GB:X12347; GB:X123.
R:Argreaves, W.S.; Deak, F.; Sparks, K.J.; Kliss, I.; Goetlinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A:Title: Structural features of cartilage matrix protein deduced from cDNA.
A:Reference number: A26364; MUID:87092429; PMID:3025875
A:Accession: A26364
A:Molecule type: mRNA
A:Residues: 78-493 <ANG>
A:Cross-references: UNIPARC:UPI000004F1EE; GB:M14792; NID:g211545; PIDN:AAA48695.1; PID:
C:Superfamily: cartilage matrix protein; BGF homology; von Willebrand factor type A repe
F:125-260/Domain: von Willebrand factor type A repeat homology <VWA1>
F:1270-434/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 14.0%; Score 490; DB 2; Length 493;
Best Local Similarity 29.6%; Pred. No. 5.2e-25;
Matches 125; Conservative 68; Mismatches 177; Indels 52; Gaps 7;

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Qy 293 D$PFI0$T$IGKRRPFIQKOLLADVNOALDIBGAPLMGVQGDNPATHPNIXHTN 352
Db 39 DLVFI0$SSVRPQEFKRVFUSRVLEGDLVGNSRVRGVINASA.VKQF$KTHQT 98
Qy 353 SRDLTAKTEKTORGL$SNVGRASIVTUKNF$SKANGRSAPN---VVVVVDMGMPDK 409
Db 99 KAEILOAVORIEPLSTGMTGLAIQFALSRAFSDTEGARLSRPNINKVAIIVTDGRPDG 158
Qy 410 VEEASRLAREGINFFI-----TIEGAENKQYVVERPNARK--AV 450
Db 159 VQDVASARARQAGIELFALGVGRVDMHTLRQIASEPLDDHVYVBSYSIEXLTHPQDAF 218
Qy 451 C-----RTNGFYSLHVQ$MFGHLKTLQPLVYKRCVCDTRLACKTCJLN 492
Db 219 CV$SDLCTGTHDCEQICISTP$SKYKACKGFTLND-----GKTC$-----AC$GSGS 269
Qy 493 SADIGFVIDGSS$VGTGNFRTVLOFVNLTYEFEISDTRIGAVQVITYEORLEBF$DKY 552
Db 270 ALDLVFLIDG$K$YVRPNFELVYKFINQIVESLEVESEKQAOVGLVQYSS$VROE$PLQF 329
Qy 553 $SKPDIINAIRVGV$SGSTG$AINFALDEL---K$K$PNK$KMLILTLDP$SYNDV 609
Db 330 NKKDIDKAIVK$KMAEM$KMTGALKYLVOS$SFIANGARGV$KVIIVTLDG$SOYI 389
Qy 610 RIPAMAHLKGVITTAIVANAMAQOELEVIATHPAR$DSFVDEFDNLIHQVVRP$RIONIC 669
Db 390 TDAKKAKADLQPRMFAVGNAVDELEINASEPVA$HYFTADPRTISNIGKLO$M$IC 449
Qy 670 TE 671
Db 450 VE 451

```

RESULT 5

060322
cartilage matrix protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S66522
R/Ascoli, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hirtl, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996
A/Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c
A/Reference number: S66522; MUID:96270751; PMID:8665920
A/Accession: S66522
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-500 <AS>
A/Cross-references: UNIPROT:P51942; UNIPARC:UPI0000029480; EMBL:U35035; NID:g1163178; P
C/Genetics:
A/Gene: CMP
C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
E.1-29/Domain: signal sequence #status predicted <SIG>
E.30-50/Product: cartilage matrix protein #status predicted <MAT>
E.43-210/Domain: von Willebrand factor type A repeat homology <WVA1>
E.231-266/Domain: EGF homology <EGF>
E.277-441/Domain: von Willebrand factor type A repeat homology <WVA2>

| | Query Match | 14.0% | Score 490; | DB 2: | Length 500; |
|----|--|--------------|--------------------|-----------------|--------------------|
| | Best Local Similarity | 28.8% | Pred. No. 5.3e-25; | | |
| | Matches 130; | Conservative | 72; | Mismatches 184; | Indels 66; Gaps 8; |
| Qy | 266 SLGVPEKEELSTQSLEPVSLDGPNCCKIDLSFLIDGSTIGKRRRIQKOLLADVAQAIDI 325 | : | : | : | : |
| Dd | 27 SLSLVPGQRGHLCRTPT-----DLIVVDSRSRVRVEEKKVYFSLQYIESLIDV 77 | : | : | : | : |
| Qy | 326 GPAPPLGVVOYGDNPAITHFNLLKTHNSRDILKIETIQRGGLSNVGRAISFYTKNFFS 385 | : : : | : | : | : |
| Dd | 78 GPNTIRVGLVNVYASTVKPEFLPRAHGSKALLQAVRRIQPLSTGMGTALQFAITAKLS 137 | : : : | : | : | : |
| Qy | 386 KANGNRSGAEN---VVVVVDUGWPPDKVKEEKSLARBESGINIFLTBGAANE--KOY 440 | : : : | : | : | : |
| Dd | 138 DAEGGRARSPIISKVIVVTIDGRPDSDRVADSEBARASGIELFAGI-L-GRDKATTLQIA 196 | : : : | : | : | : |

[illegible]

RESULT 6

collagen alpha (VI) chain precursor [validated] - human
N.Contains: collagen alpha 3(VI) chain, splice form A3/N10(-)
C.Species: Homo sapiens (man)
C.Date: 21-Nov-1993 #sequence, revision 12-Nov-1999 #text, change 16-Aug-2004
C.Accession: A59140; S13679; S24465; A57083; S28776; S00245; C31952; C29848; S26510; S48100
R.Chu, M.L.
submitted to GenBank, May 1998
A.Reference number: A59140
A.Accession: A59140
A.Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-3176 <CH>
A.Cross-references: UNIPROT:P12111; UNIPARC:UPI0000126D4F; GB:X52022; NID:G3127925; PIDN:R.Chu, M.L.; Zhang, R.Z.; Pan, T.; Stokes, D.; Conway, D.; Kuo, H.T.; Glanville, R.; Mayne, E.MBO J. 9, 385-393, 1990
A.Title: Mosaic structure of globular domains in the human type VI collagen alpha-3 chain
A.Reference number: S13679; MUID:90151612; PMID:1689238
A.Accession: S13679
A.Molecule type: mRNA
A.Residues: 1-30,227-313 'CWW', 318-322, 'AR', 326-1815, 'FD', 1818-1819, 'ID', 1822-3176 <CH5>
A.Cross-references: UNIPARC:UPI0000173C14; EMBL:X52022; NID:G3127925
A.Accession: S24465
A.Molecule type: protein
A.Residues: 574-585;965-973, 'X', 975-976;1306-1325;1361-1377;1381-1401;1473-1506, 'X', 1508-1562, 'X', 1564-1965;2018-2037;2374-2410;2445-2459;2466-2469, 'X', 2471-2474;2504-2508, 'X', 2509-2510;2511-2512;2513-2514;2515-2516;2517-2518;2519-2520;2521-2522;2523-2524;2525-2526;2527-2528;2529-2530;2531-2532;2533-2534;2535-2536;2537-2538;2539-2540;2541-2542;2543-2544;2545-2546;2547-2548;2549-2550;2551-2552;2553-2554;2555-2556;2557-2558;2559-2560;2561-2562;2563-2564;2565-2566;2567-2568;2569-2570;2571-2572;2573-2574;2575-2576;2577-2578;2579-2580;2581-2582;2583-2584;2585-2586;2587-2588;2589-2590;2591-2592;2593-2594;2595-2596;2597-2598;2599-2600;2601-2602;2603-2604;2605-2606;2607-2608;2609-2610;2611-2612;2613-2614;2615-2616;2617-2618;2619-2620;2621-2622;2623-2624;2625-2626;2627-2628;2629-2630;2631-2632;2633-2634;2635-2636;2637-2638;2639-2640;2641-2642;2643-2644;2645-2646;2647-2648;2649-2650;2651-2652;2653-2654;2655-2656;2657-2658;2659-2660;2661-2662;2663-2664;2665-2666;2667-2668;2669-2670;2671-2672;2673-2674;2675-2676;2677-2678;2679-2680;2681-2682;2683-2684;2685-2686;2687-2688;2689-2690;2691-2692;2693-2694;2695-2696;2697-2698;2699-2700;2701-2702;2703-2704;2705-2706;2707-2708;2709-2710;2711-2712;2713-2714;2715-2716;2717-2718;2719-2720;2721-2722;2723-2724;2725-2726;2727-2728;2729-2730;2731-2732;2733-2734;2735-2736;2737-2738;2739-2740;2741-2742;2743-2744;2745-2746;2747-2748;2749-2750;2751-2752;2753-2754;2755-2756;2757-2758;2759-2760;2761-2762;2763-2764;2765-2766;2767-2768;2769-2770;2771-2772;2773-2774;2775-2776;2777-2778;2779-2780;2781-2782;2783-2784;2785-2786;2787-2788;2789-2790;2791-2792;2793-2794;2795-2796;2797-2798;2799-2800;2801-2802;2803-2804;2805-2806;2807-2808;2809-2810;2811-2812;2813-2814;2815-2816;2817-2818;2819-2820;2821-2822;2823-2824;2825-2826;2827-2828;2829-2830;2831-2832;2833-2834;2835-2836;2837-2838;2839-2840;2841-2842;2843-2844;2845-2846;2847-2848;2849-2850;2851-2852;2853-2854;2855-2856;2857-2858;2859-2860;2861-2862;2863-2864;2865-2866;2867-2868;2869-2870;2871-2872;2873-2874;2875-2876;2877-2878;2879-2880;2881-2882;2883-2884;2885-2886;2887-2888;2889-2890;2891-2892;2893-2894;2895-2896;2897-2898;2899-2900;2901-2902;2903-2904;2905-2906;2907-2908;2909-2910;2911-2912;2913-2914;2915-2916;2917-2918;2919-2920;2921-2922;2923-2924;2925-2926;2927-2928;2929-2930;2931-2932;2933-2934;2935-2936;2937-2938;2939-2940;2941-2942;2943-2944;2945-2946;2947-2948;2949-2950;2951-2952;2953-2954;2955-2956;2957-2958;2959-2960;2961-2962;2963-2964;2965-2966;2967-2968;2969-2970;2971-2972;2973-2974;2975-2976;2977-2978;2979-2980;2981-2982;2983-2984;2985-2986;2987-2988;2989-2990;2991-2992;2993-2994;2995-2996;2997-2998;2999-3000;3001-3002;3003-3004;3005-3006;3007-3008;3009-3010;3011-3012;3013-3014;3015-3016;3017-3018;3019-3020;3021-3022;3023-3024;3025-3026;3027-3028;3029-3030;3031-3032;3033-3034;3035-3036;3037-3038;3039-3040;3041-3042;3043-3044;3045-3046;3047-3048;3049-3050;3051-3052;3053-3054;3055-3056;3057-3058;3059-3060;3061-3062;3063-3064;3065-3066;3067-3068;3069-3070;3071-3072;3073-3074;3075-3076;3077-3078;3079-3080;3081-3082;3083-3084;3085-3086;3087-3088;3089-3090;3091-3092;3093-3094;3095-3096;3097-3098;3099-3100;3101-3102;3103-3104;3105-3106;3107-3108;3109-3110;3111-3112;3113-3114;3115-3116;3117-3118;3119-3120;3121-3122;3123-3124;3125-3126;3127-3128;3129-3130;3131-3132;3133-3134;3135-3136;3137-3138;3139-3140;3141-3142;3143-3144;3145-3146;3147-3148;3149-3150;3151-3152;3153-3154;3155-3156;3157-3158;3159-3160;3161-3162;3163-3164;3165-3166;3167-3168;3169-3170;3171-3172;3173-3174;3175-317

A>Note: the mRNA portion of the sequence corresponds to residues 2092-2157
 J.Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; Deutmman, R.; Timpl, R.
 J. Biol. Chem. 263, 18601-18606, 1988
 A>Title: Amino acid sequence of the triple-helical domain of human collagen type VI.
 A:Reference number: A31952; MUID:89066644; PMID:3198591
 A:Accession: C31952
 A:Molecule type: mRNA
 A:Residues: 2038-2373 <CH4>
 A:Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778
 A>Note: parts of this sequence were determined by protein sequencing
 R.Well, D.; Mattei, M.G.; Passase, E.; Van Cong, N.; Pribula-Conway, D.; Mann, K.; Deutz
 Am. J. Hum. Genet. 42, 435-445, 1988
 A>Title: Cloning and chromosomal localization of human genes encoding the three chains C
 A:Reference number: A29848; MUID:88161046; PMID:3348212
 A:Accession: C29848
 A:Molecule type: mRNA
 A:Residues: 2032-2151 <WE1>
 A:Cross-references: UNIPARC:UPI000016A720; GB:M27449; NID:9291919; PIDN:AA52057.1; PID:
 A>Note: part of this sequence was determined by protein sequencing
 R.Jander, R.; Rautenberg, J.; Gianville, R.W.
 Eur. J. Biochem. 133, 39-46, 1983
 A>Title: Further characterization of the three polypeptide chains of bovine and human sh
 A:Reference number: S26506; MUID:83209648; PMID:6852033
 A:Accession: S26510
 A:Molecule type: Protein
 A:Residues: 'SALAGVAGV' <JAN>
 A:Cross-references: UNIPARC:UPI0000173C2F
 A>Note: this sequence cannot be reliably placed and probably represents the results from
 R.Mayer, J.; Poeschl, E.; Nisch, R.; Specks, U.; Pan, T.C.; Chu, M.L.; Timpl, R.
 Eur. J. Biochem. 225, 573-580, 1994
 A>Title: Recombinant expression and properties of the kunitz-type protease-inhibitor mod
 A:Reference number: S48709; MUID:95045506; PMID:7525281
 A:Accession: S48709
 A:Molecule type: mRNA
 A:Residues: 'KRAWIFFLCLAGRALAA', 3102-3176 <MAY>
 A:Cross-references: UNIPARC:UPI0000173C30
 A>Note: engineered sequence to allow isolation of the kunitz-type proteinase inhibitor h
 R.Arroux, B.; Merigean, K.; Saladjian, P.; Norris, F.; Norris, K.; Bjorn, S.; Olsen, O.;
 submitted to the Brookhaven Protein Data Bank, August 1994
 A:Reference number: A52812; PDB:1KNT
 A:Contents: annotation; X-ray crystallography, 1.6 angstroms, residues 3106-3160
 A>Note: engineered sequence expressed in Saccharomyces cerevisiae strain mc-663
 C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
 lines are 5-hydroxylated and subsequently O-glycosylated.
 C:Comment: The fibronectin type III repeat homology domain may be released during proces
 C:Genetics:
 A:Gene: GDB:COL6A3
 A:Cross-references: GDB:119066; OMIM:120250
 A:Map position: 2q37.3-2q37.3
 C:Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUA),
 sociations among trimer amino- and carboxyl-terminal domains (with disulfide bonds).
 C:Function:
 A:Description: structural component of extracellular tissue microfibrils associated with
 C:Superfamily: collagen VI
 C:Keywords: alternative splicing; blocked amino end; cell binding; coiled coil; extracel
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-3176/Product: collagen alpha 3(VI) chain #status predicted <MAT>
 F:26-2037/Domain: amino-terminal nonhelical #status predicted <ANH>
 F:26-30-2373/Product: collagen alpha 3(VI) chain, splice form A9/N10(-) #status pred
 F:37-203/Domain: von Willebrand factor type A repeat homology <VM01>
 F:240-405/Domain: von Willebrand factor type A repeat homology <VM02>
 F:443-608/Domain: von Willebrand factor type A repeat homology <VM03>
 F:637-802/Domain: von Willebrand factor type A repeat homology <VM04>
 F:835-999/Domain: von Willebrand factor type A repeat homology <VM05>
 F:1027-1191/Domain: von Willebrand factor type A repeat homology <VM06>
 F:1231-1394/Domain: von Willebrand factor type A repeat homology <VM07>
 F:1434-1599/Domain: von Willebrand factor type A repeat homology <VM08>
 F:1637-1802/Domain: von Willebrand factor type A repeat homology <VM09>
 F:1836-2005/Domain: von Willebrand factor type A repeat homology <VM10>
 F:2038-2373/Region: interrupted helical
 F:2040-2042/Region: cell attachment (R-G-D) motif
 F:2136-2138/Region: cell attachment (R-G-D) motif
 F:2148-2150/Region: cell attachment (R-G-D) motif

F:2154-2156/Region: cell attachment (R-G-D) motif
 F:2370-2372/Region: cell attachment (R-G-D) motif
 F:2374-3176/Domain: carboxyl-terminal nonhelical #status predicted <CNH>
 F:2400-2571/Domain: von Willebrand factor type A repeat homology <VM11>
 F:2617-2800/Domain: von Willebrand factor type A repeat homology <VM12>
 F:2865-2986/Region: alanine/lysine/proline/threonine/valine-rich repeats
 F:2987-3072/Domain: fibronectin type III repeat homology <FN3>
 F:3111-3161/Domain: animal kunitz-type proteinase inhibitor homology <BP1>
 F:326/Modified site: pyrolysine carboxylic acid (Gln) (in mature form) #status predicted
 F:106,116,202,251,2079,2331,2558,2677,2861,3036/Binding site: carbohydrate (Asn) (covalen
 F:2087/Disulfide bonds: interchain #status predicted
 F:2100,2206,2239,2316,2319/Modified site: 4-hydroxyproline (Pro) #status experimental
 F:2103,2209,2212,2322,2337/Binding site: carbohydrate (Lys) (covalent) #status experimen
 F:2103,2209,2212,2322,2337/Modified site: 5-hydroxylysine (Lys) #status experimental
 F:3111-3161,3120-3144,3136-3157/Disulfide bonds: #status predicted
 Query Match 13.5%; Score 471.5; DB 2; Length 3176;
 Best Local Similarity 30.9%; Pred. No. 1.5e-22;
 Matches 122; Conservative 86; Mismatches 148; Indels 39; Gaps 12;
 QY 293 DLSFLDSTSGIKRRPRIOKQLADVAQADIGPAGLMGVGYGDNPATHPNLTHTN 352
 DB 39 DIFLVDSSTWITGEHFVLRFLYDVVKSIAVGBNDPFLVQPNPHTFELNITRT 98
 QY 353 SRDLTALEKITORGSLSNVGRALSFYKNEFSKANGNR--GAPNVVVVWDGWPFDKV 410
 DB 99 KQVLSHSHSNMSYIGTNGTQKGLGYIMQSHLTAAAGRAGDGPQVIVLTDGHSKGL 158
 QY 411 EASRLARESGINIFITTEGAENE-KQVVEPFPANKAVCRITNGFYSLL--VQSWFG- 466
 DB 159 ALPSLELKSADVNFALIGVEDADGALKEISEP--LMHFNFNLNFTSLHDYGNLVSC 216
 QY 467 LKHTQLPIVKRCVCTDRLACSKTCLNSADIGFVIDGSSVSGTGPRTVLTQVTLTKFE 526
 DB 217 VHSVSP--ERAGDLETIK-DITQDSADILFLIDGSNNNTSVNPAVLIDFLVNLKLP 273
 QY 527 ISDTDTRIGAVQYTYEORLEFPDKYSKSPDILNAIKRVGWSGQ--TSTGAINFALQ 584
 DB 274 IGTQIRGVGVQFSDERPMTSLDTYSTKAVLQVAVLGR-AGGELANIGLADPFVEN 332
 QY 585 LFKSKPKNKK---RKLMLITDGRSYDDVRIIPMAAHLKQVITYAIGVAMAQEELEVI 639
 DB 333 HFTAGSGRVEGEPQVVLVLSAGPSSDEIRYGVAVLQKQASVFSGLGAQASRAELQHI 392
 QY 640 ATHPARDSFFVDFPDNLHQVVPRIIONICRTEFNS 674
 DB 393 ATD-----DNLVFTVP-----EPRS 407
 RESULT 7
 S31212
 collagen alpha 1(XIV) chain precursor, short form - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
 C:Accession: S31212
 R.Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
 Eur. J. Biochem. 212, 483-490, 1993
 A>Title: Complete primary structure of chicken collagen XIV.
 A:Reference number: S31211; MUID:93185668; PMID:8444186
 A:Accession: S31212
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-1857 <NAE>
 A:Cross-references: UNIPARC:UPI000017123C; EMBL:X70792; NID:9288974; PIDN:CAA50063.1; PI
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 C:Genetics:
 A:Gene: COL14A1
 C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
 F:129-110/Domain: fibronectin type III repeat homology <FN3A>
 F:156-330/Domain: von Willebrand factor type A repeat homology <VM1>
 F:352-433/Domain: fibronectin type III repeat homology <FN3B>

F:442-525/Domain: fibronectin type III repeat homology <FN3C>
 F:534-614/Domain: fibronectin type III repeat homology <FN3D>
 F:623-707/Domain: fibronectin type III repeat homology <FN3E>
 F:741-823/Domain: fibronectin type III repeat homology <FN3F>
 F:832-914/Domain: fibronectin type III repeat homology <FN3G>
 F:922-1009/Domain: fibronectin type III repeat homology <FN3H>
 F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 9.5%; Score 311; DB 2; Length 1857;
 Best Local Similarity 24.8%; Pred. No. 1.7e-13;
 Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

Qy 174 IPGTTAQPVTLMQLAVTVAAPTTLPRSPSAASTSTIPRQSGHRSQEMD----- 227
 Db 713 IVGTTALPTT-----VTTTTTATTPKPTIAVFR-----GVRNLVIDDETTSS 757
 Qy 228 ---LMSATYTYSSQNR-----PRADPGIORODPSGAAPKPVGADVSLGLVPKEELS 276
 Db 758 LRVVWDISDHAQOFRVTYTLAKGDRAEALMPGRQNTLLQP-----LLPDTREYK 809
 Qy 277 TQSL-----EPVSLGDPNCKIDLSFLIDGSTSIGRRFRIOKOLADVQAALDIDGAPG 330
 Db 810 VTTPRIYADGCVSAAGKTLPLS-----APRNLRVSDWYNNRLKISWD-APRSP 859
 Qy 331 LMG--VVQYGDN---PATFNLKTHNTSRDLKTAIEKTORGGLSNVGRALSFVTKNFFS 385
 Db 860 TMGRIRIVKSIINVGPA---LETFVGD-DINTIL-----ILNLFSGTEYSVKVPAS 906
 Qy 386 KANG---NRSGAPVVVVVWDGWPPTDKVEASRLAR---ESGINIFFITTEGAENEMKQY 439
 Db 907 YSTGFSALGVAKTLVGLVNTDYGVRMTSLCAQOLRHATATVAVIESLVDGKKQ- 965
 Qy 440 VVEBNFANKAVCRTNGYSL--HVQSWFGLHKTLO----- 472
 Db 966 --EVNLGG-GVPR-HCFEELMPGTEYKISVHAQOEIEGPAVSIMETTLPPPTQPTSPS 1021
 Qy 473 -----PLVKRYCDTRLACSKTCLNSADIGVIDSSSVGNGNFRVTLQFVTNLTKE 524
 Db 1022 TTLPPPTIPPAKEVCKAAK-----ADLVFLVDGSMISGDDNFNKIISFLYSVGA 1071
 Qy 525 FE-ISDTRTIGAVQYTYEORLEFGPDYSSKPDILNAIKRVGWYSGTSGAIAINFAL 583
 Db 1072 LDKTGPDTQVAIIQFSDPRTPEFLNAYKTETLLEAIQOIAVKGNTTGAIAIKHARE 1131
 Qy 584 QLF-----KSKRNKRKMLITTDGRSYDDVRIIPAMAHLKGVITVAIGVAMAQOELE 637
 Db 1132 VLFEGAGMKRGIP---KVLVVIITDGRSQDDVNVKVRMQLDGFSPFALIGVADADYSELV 1188
 Qy 638 VIATHPARDSFFVDFEDNHLQVPRITIQNIC 669
 Db 1189 NIGSKPESRHHVFVDPDFDAFTKIEDLITFVC 1220

RESULT 8

collagen alpha 1(XIV) chain precursor, long form - chicken

C/Species: Gallus gallus (chicken)

C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004

C/Accession: S78476; S31211

R/Tueb, B.

submitted to the EMBL Data Library, January 1993

A/Reference number: S78476

A/Accession: S78476

A/Molecule type: mRNA

A/Residues: 1-1888 <TRU>

A/Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; NID:G288872; PTC

R/Weichl, C.; Tueb, J.; Kessler, B.; Winterhalter, K.H.; Tueb, B.

Eur. J. Biochem. 212, 483-490, 1993

A/Title: Complete primary structure of chicken collagen XIV.

A/Reference number: S31211; MUID:93185668; PMID:844186

A/Accession: S31211

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-416/1460-1811, 1843-1888 <WAE>
 A/Cross-references: UNIPARC:UPI00001773F4; UNIPARC:UPI00001773F5; EMBL:X70793
 C/Genetics:
 A/Gene: Coll14A1
 C/Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:129-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
 F:129-110/Domain: fibronectin type III repeat homology <FN3A>
 F:156-330/Domain: von Willebrand factor type A repeat homology <VWA1>
 F:325-433/Domain: fibronectin type III repeat homology <FN3B>
 F:442-525/Domain: fibronectin type III repeat homology <FN3C>
 F:534-614/Domain: fibronectin type III repeat homology <FN3D>
 F:623-707/Domain: fibronectin type III repeat homology <FN3E>
 F:741-823/Domain: fibronectin type III repeat homology <FN3F>
 F:832-914/Domain: fibronectin type III repeat homology <FN3G>
 F:922-1009/Domain: fibronectin type III repeat homology <FN3H>
 F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 9.5%; Score 311; DB 2; Length 1888;
 Best Local Similarity 24.8%; Pred. No. 1.7e-13;
 Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

Qy 174 IPGTTAQPVTLMQLAVTVAAPTTLPRSPSAASTSTIPRQSGHRSQEMD----- 227
 Db 713 IVGTTALPTT-----VTTTTTATTPKPTIAVFR-----GVRNLVIDDETTSS 757
 Qy 228 ---LMSATYTYSSQNR-----PRADPGIORODPSGAAPKPVGADVSLGLVPKEELS 276
 Db 758 LRVVWDISDHAQOFRVTYTLAKGDRAEALMPGRQNTLLQP-----LLPDTREYK 809
 Qy 277 TQSL-----EPVSLGDPNCKIDLSFLIDGSTSIGRRFRIOKOLADVQAALDIDGAPG 330
 Db 810 VTTPRIYADGCVSAAGKTLPLS-----APRNLRVSDWYNNRLKISWD-APRSP 859
 Qy 331 LMG--VVQYGDN---PATFNLKTHNTSRDLKTAIEKTORGGLSNVGRALSFVTKNFFS 385
 Db 860 TMGRIRIVKSIINVGPA---LETFVGD-DINTIL-----ILNLFSGTEYSVKVPAS 906
 Qy 386 KANG---NRSGAPVVVVVWDGWPPTDKVEASRLAR---ESGINIFFITTEGAENEMKQY 439
 Db 907 YSTGFSALGVAKTLVGLVNTDYGVRMTSLCAQOLRHATATVAVIESLVDGKKQ- 965
 Qy 440 VVEBNFANKAVCRTNGYSL--HVQSWFGLHKTLO----- 472
 Db 966 --EVNLGG-GVPR-HCFEELMPGTEYKISVHAQOEIEGPAVSIMETTLPPPTQPTSPS 1021
 Qy 473 -----PLVKRYCDTRLACSKTCLNSADIGVIDSSSVGNGNFRVTLQFVTNLTKE 524
 Db 1022 TTLPPPTIPPAKEVCKAAK-----ADLVFLVDGSMISGDDNFNKIISFLYSVGA 1071
 Qy 525 FE-ISDTRTIGAVQYTYEORLEFGPDYSSKPDILNAIKRVGWYSGTSGAIAINFAL 583
 Db 1072 LDKTGPDTQVAIIQFSDPRTPEFLNAYKTETLLEAIQOIAVKGNTTGAIAIKHARE 1131
 Qy 584 QLF-----KSKRNKRKMLITTDGRSYDDVRIIPAMAHLKGVITVAIGVAMAQOELE 637
 Db 1132 VLFEGAGMKRGIP---KVLVVIITDGRSQDDVNVKVRMQLDGFSPFALIGVADADYSELV 1188
 Qy 638 VIATHPARDSFFVDFEDNHLQVPRITIQNIC 669
 Db 1189 NIGSKPESRHHVFVDPDFDAFTKIEDLITFVC 1220

RESULT 9

collagen alpha 1(VII) chain precursor - human

N/Alternate names: procollagen alpha 1(VII) chain

C/Species: Homo sapiens (man)

C/Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004

C/Accession: A54849; PH0844; S16316; I56328; A30296; I84686

R/Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.

J. Biol. Chem. 269, 20256-20262, 1994

A/Title: Cloning of human type VII collagen. Complete primary sequence of the alpha(VII)

A:Reference number: A54849; MUID:94327588; PMID:8051117
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2944 <CHR>
A:Cross-references: UNIPROT:Q02388; UNIPARC:UPI000017A138; GB:L02870; NID:9987124; PIDN:R1tanak.T.; Takahashi, K.; Furukawa, F.; Imanura, S.
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
A:Title: Molecular cloning and characterization of type VII collagen cDNA.
A:Reference number: PH0844; MUID:92231902; PMID:1567409
A:Accession: PH0844
A:Molecule type: mRNA
A:Residues: 'EPR',340-475, 'RAUSTASHSTLCWATRWHPGRCGSHWTRAPACEPCNRPASHRAARAG',524-528, 'C',
A:Cross-references: UNIPARC:UPI000017A139; DDBJ:D11152; DDBJ:D13694; NID:9453698; PIDN:E
A:Experimental source: Keratinocyte
A:Note: The authors translated the codon ACC for residues 394 and 397 as Tyr
R:Parente, M.G.; Chung, L.C.; Rymaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat
proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A:Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A:Reference number: S16316; MUID:91334380; PMID:1871109
A:Accession: S16316
A:Molecule type: mRNA
A:Residues: 815-892, 'E', 894-1439 <PAR>
A:Cross-references: UNIPARC:UPI000016A722; GB:M65158; GB:S49017; NID:9180914; PIDN:AAA98
A:Experimental source: keratinocyte
R:Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Priyaanah, P.S.; Cook, M.E.; Wright, J.
J. Invest. Dermatol. 99, 691-696, 1992
A:Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prob
A:Reference number: I56328; MUID:93107742; PMID:1469284
A:Accession: I56328
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'EPR',312-517, 'DV',520-540, 'W',542-1255 <RES>
A:Cross-references: UNIPARC:UPI000016B3AC; GB:S51236; NID:9262308; PIDN:AAB24637.1; PID
R:Selzler, J.L.; Eisten, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E.
J. Biol. Chem. 264, 3822-3825, 1989
A:Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagenase
A:Reference number: A30296; MUID:89139437; PMID:2537292
A:Accession: A30296
A:Molecule type: protein
A:Residues: 'A',1240-1246, 'G',1248-1250, 'XE',1253-1255, 'Q',1257, 'E',2032, 'C',2034-2041, 'H
A:Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C.
A:Note: two reported peptides cannot be reliably located
R:Greenspan, D.S.
Hum. Mol. Genet. 2, 273-278, 1993
A:Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A:Reference number: I48103; MUID:93271985; PMID:8499916
A:Accession: I48103
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 2395-2871, 'S',2873-2944 <RES>
A:Cross-references: UNIPARC:UPI000016A724; GB:L06862; NID:9388713; PIDN:AAA89196.1; PID
R:Christiano, A.M.; Rymaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A:Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser substitution
A:Reference number: A55255; MUID:94224777; PMID:8170945
A:Contents: annotation
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit (Gly-P
ed and subsequently O-glycosylated.
C:Genetics: GDB:COL7A1; EBR1; EBD1; EB
A:Gene: GDB:COL7A1; EBR1; EBD1; EB
A:Cross-references: GDB:128750; OMIM:120120
A:Map position: 3p21.3-3p21.3
A:Note: defects in this gene can result in dominant and recessive dystrophic epidermolysis
C:Complex: type VII collagen is probably a homotrimer
C:Function:
A:Description: structural component of extracellular polymer associated with anchoring fibrils
C:Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproline
F:17-1253/Product: collagen alpha 1(VII) chain #status predicted <MAT>
F:17-1253/Product: collagen alpha 1(VII) chain #status predicted <NC1>
F:36-201/Domain: von Willebrand factor type A repeat homology <VWA1>

Query Match
Best Local Similarity 9.4%; Score 329.5; DB 2; Length 2944;
Matches 80; Conservative 37; Mismatches 88; Indels 19; Gaps 4;

Qy 470 TIQPLVKRC-----DTRLRCKSTCLNSADIGFVIDSSVGTGNFRYTLQ 516
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 2 TIRLIVALLCAGLIAAPRYARQHREKVTCTR--LYADIYFLDDGSSISGRNPREFRS 59

Qy 517 FVTNLTKERE-ISTDTIRIGAVOYTYEQRLERFGFKYSKPDIILAIKRGVWSGGTST 574
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 60 FLEGVLPSGSAASQGVPRATVOYSDPRTREFGLDALSGSGVIYAIRIELSYKCGNTRT 119

Qy 575 GAALNALQLP--KSKPKRKLMILITDGSRSDVDVRIPMAAHLKGVITYAIGVAAA 632
| | | | | | | | | | | | | | | | | | | | | | : | : | : | : | : | : | :
Db 120 GAAILHVAHVHFPPOLARPDPVPVCILITDGKSDDLVDTAQRLLKGQGVKLFAVGIKRAD 179

Qy 633 QEELEVIATHPARDHSFVDEFDNLHOYVPIRIIONICTEFNSQP 676
| | | | | | | | | | | | | | | | | | | | | | : | : | : | : | : | : | :
Db 180 PEEELKVVASQPTSDFFPVNDPFSLRTLPLVRSRVCTTAGGPV 223

RESULT 10

A45974
collagen alpha 1 (XIV) chain precursor, short form 2 - chicken
N.Alternate names: undulin
C.Species: Gallus gallus (chicken)
C.Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: A45974, S30085, S22916, S17035, S20833
R.Gercke, D.R.; Foley, J.W.; Castagnola, P.; Gemari, M.; Dublet, B.; Cancedda, R.; Llin
J. Biol. Chem. 268, 12177-12184, 1993
U.Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
ns.

A.Reference number: A45974; WUID:93280195; PMID:8505337
A.Accession: A45974
A.Status: preliminary
A.Molecule type: mRNA, protein
A.Residues: 1-1747 <GER>
A.Cross-references: UNIPROT:P32018; UNIPARC:UPI0000173C47
A.Experimental source: embryo skin
A.Note: sequence inconsistent with the nucleotide translation
A.Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
R.Appe, S.S.
submitted to the EMBL Data Library, March 1992
A.Reference number: S30085
A.Accession: S30085
A.Molecule type: mRNA
A.Residues: 1472-1660 <APT>
A.Cross-references: UNIPARC:UPI00000006A2; EMBL:X65122; NID:g62871; PIDN:CAA46238.1; PID
R.Trieb, J.; Trieb, B.

Ent. J. Biochem 207, 549-557, 1992

Article: Type XIV collagen is a variant of undulin.

Reference number: S22916; MUID:92339443; PMID:1339349

A:Accession: S22916

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 286-497, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>

A:Cross-references: UNIPARC:UPI0000173C48

R:Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsmeijer, T.F.; van der Rest, M.; Mayne, Eur. J. Biochem. 201, 333-339, 1991

Article: Cloning of a cDNA for a new member of the class of fibril-associated collagens

A:Reference number: S17035; MUID:92037585; PMID:1935930

A:Accession: S17035

A:Molecule type: mRNA

A:Residues: 1472-1659 <GOR1>

A:Cross-references: UNIPARC:UPI0000173C49

A:Accession: S20833

A:Molecule type: protein

A:Residues: 1551-1570, 1593-1639, 1639-1667 <GOR2>

A:Cross-references: UNIPARC:UPI0000173C49

C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimers

F:40-204/Domain: von Willebrand factor type A repeat homology <WMA1>

F:236-317/Domain: fibronectin type III repeat homology <FNA3>

F:326-409/Domain: fibronectin type III repeat homology <FNA3B>

F:418-498/Domain: fibronectin type III repeat homology <FNA3C>

F:507-591/Domain: fibronectin type III repeat homology <FNA3D>

F:625-707/Domain: fibronectin type III repeat homology <FNA3E>

F:716-798/Domain: fibronectin type III repeat homology <FNA3F>

F:806-893/Domain: fibronectin type III repeat homology <FNA3G>

F:924-1089/Domain: von Willebrand factor type A repeat homology <VMA2>

F:1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>

F:1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>

F:1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 9.4%; Score 329; DB 2; Length 1747;

Best local similarity 24.8%; Pred. No. 2e-13;

Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

QY 174 IPGTTAQVPTLMQLLAVTAVAATPTLPRPSPSAATSTISRPPOSVGHRSQEMD----- 227

DB 597 IVGTALPFT-----VTTTTTTATYTPKPTIAVFT-----GVRNLVIDDETSS 641

QY 228 ---LMSTATYSSQNR-----PRADPGIQRDPSGAARQKPYGADVSLGLVPKRELS 276

DB 642 LRVWDVDSIDHNAQQRVTVYTLAKGDRAEALINVERQNTLLLP-----LIPDTEYK 693

QY 277 TQSL-----EPVSGIDPNCKIDISFLIDGSTSIGKRFRRIQKQLLDVAQALDIGAPG 330

DB 694 VTTPITYADGEGVSASAPGKTLPLS-----APRLRVSDSEMYNRLRISWD-APPSF 743

QY 331 LMG--VVOYQDN---PAHFNLKHTNSRDLTALAEKLTQGGSLSNVRAISPTXKFFS 385

DB 744 TMGYRIYKVSINVPGRPA---LETFVGD-DINTTL-----ILNLSGTEYSVKVFA 790

QY 386 KANG---NRSQAPNVVVVWDGMPFDKVEEASRLAR---ESSGINFTTIGCAENEKQY 439

DB 791 YSTGSDSLTYGAKTLYGATNLDTYOVRMTSLCQNMQLHRAHRYRIVVIESLYDGKKQ- 849

QY 440 VPEPNFANKAVCRITNGFYSL---HVQSWFGLKHTIQ----- 472

DB 850 --EVLILG-GVPR-HCFELMFGTEYKLSVHAQLOEIGPAPVSINETLLPPTPTPTSPS 905

QY 473 -----PLVKRYVDPTDLRACSKTCLNSADIGFPIIDSSSSVGNPNFTVLOPNTLKE 524

DB 956 LDKIGPDGTQVAIIQFDSDPRTEFKLANVKTRETLLEAIQGLAVYGGTQTKGAIKARE 1015

QY 584 QLF-----KSKPKRKLTMLITDGRSYDDVRIPAMAHLKGVITTAIGVAMAQDELTE 637

DB 1016 VLFGEAGMRKGIIP---KVLVVTIDGRSQDDVNKVSREMQLDGSFPAIIGVADADYSELV 1072

[illegible]

A/Cross-references: UNIPARC:UPI000016B30B; GB:M60675; NID:g340357; PIDN:AAA61295.1; PID:
 A/Note: The authors translated the codon CGC for residue 156 as Gln
 R/Collins, C.J.; Underhill, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagian,
 Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987
 A/Title: Molecular cloning of the human gene for von Willebrand factor and identification
 A/Reference number: 523676; MUID:87260814; PMID:3496594
 A/Molecule type: DNA
 A/Accession: 523676
 A/Residues: 2731-2813 <COL>
 A/Cross-references: UNIPARC:UPI000014240A; EMBL:M16945
 R/Bonthron, D.; Orr, E.C.; Miletch, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.
 Nucleic Acids Res. 14, 7125-7127, 1986
 A/Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.
 A/Reference number: A25298; MUID:87016349; PMID:3489923
 A/Accession: A25298
 A/Molecule type: mRNA
 A/Residues: 1-470, 'V', 472-2813 <BON>
 A/Cross-references: UNIPARC:UPI000017431B; EMBL:X04385
 R/Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
 EMBO J. 5, 1839-1847, 1986
 A/Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protei
 A/Reference number: A91044; MUID:87004550; PMID:3019665
 A/Accession: A25469
 A/Molecule type: mRNA
 A/Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>
 A/Cross-references: UNIPARC:UPI000017431C; EMBL:X04146
 R/Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
 EMBO J. 5, 1839-1847, 1986
 A/Note: this sequence has been revised in reference A91056
 R/Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
 EMBO J. 5, 3074, 1986
 A/Reference number: A91056
 A/Accession: A25366
 A/Molecule type: mRNA
 A/Residues: 1021-1030 <VE2>
 A/Cross-references: UNIPARC:UPI000017431D
 A/Note: this is a revision to the sequence from reference A91044
 R/Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.
 Biochem. Biophys. Res. Commun. 144, 657-665, 1987
 A/Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated
 A/Reference number: 523618; MUID:87213253; PMID:3495266
 A/Accession: 523618
 A/Molecule type: mRNA
 A/Residues: 1-120 <SH2>
 A/Cross-references: UNIPARC:UPI000016B30A; EMBL:M17588; NID:g799330; PIDN:AAA65940.1; PI
 A/Accession: 523645
 A/Molecule type: protein
 A/Residues: 23-56 <SH3>
 A/Cross-references: UNIPARC:UPI000017431E
 R/Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.W
 Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985
 A/Title: Cloning and characterization of two cDNAs coding for human von Willebrand fact
 A/Reference number: A94060; MUID:86016708; PMID:2864688
 A/Accession: A94060
 A/Molecule type: mRNA
 A/Residues: WA, 739, 'C', 744-769, 'H', 771-788, 'A', 790-803, 'S', 805-873, 1289-1471, 'D', 1473-
 A/Cross-references: UNIPARC:UPI000017431F; UNIPARC:UPI0000174320
 A/Note: the authors translated the codon TCG for residue 2168 as Cys
 R/Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.
 Biochemistry 25, 3164-3171, 1986
 A/Title: cDNA sequences for human von Willebrand factor reveal five types of repeated dc
 A/Reference number: A90504; MUID:86265894; PMID:3488076
 A/Accession: A90504
 A/Molecule type: mRNA
 A/Residues: 781-788, 'A', 790-1424 <SHE>
 A/Cross-references: UNIPARC:UPI0000174321
 R/Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.; C
 Science 228, 1401-1406, 1985
 A/Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clones
 A/Reference number: A44178; MUID:85244588; PMID:3874428
 A/Accession: A44178
 A/Molecule type: mRNA
 A/Residues: 2821-2813 <GIN>
 A/Cross-references: UNIPARC:UPI000016B307; EMBL:K03028; NID:g340308; PIDN:AAA61293.1; PI

R/Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; van
 Nucleic Acids Res. 13, 4699-4717, 1985
 A/Title: Construction of cDNA coding for human von Willebrand factor using antibody probe
 A/Reference number: 507363; MUID:85269603; PMID:3875078
 A/Accession: 507363
 A/Molecule type: mRNA
 A/Residues: 2731-2813 <VE3>
 A/Cross-references: UNIPARC:UPI000014240A; EMBL:X02672; NID:g37939; PIDN:CAA26503.1; PID
 R/Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Living
 Cell 41, 49-56, 1985
 A/Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by a r
 A/Reference number: 523678; MUID:85201687; PMID:3873280
 A/Accession: 523678
 A/Molecule type: protein
 A/Residues: 2731-2813 <LYN>
 A/Cross-references: UNIPARC:UPI000014240A; EMBL:X03028
 R/Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.;
 Biochemistry 25, 3171-3184, 1986
 A/Title: Amino acid sequences of human von Willebrand factor.
 A/Reference number: A90505; MUID:86269895; PMID:3524673
 A/Accession: A90505
 A/Molecule type: protein
 A/Residues: 764-788, 'A', 790-1471, 'D', 1473-2813 <TIT>
 A/Cross-references: UNIPARC:UPI0000174322
 A/Note: 789-Thr was also found
 R/Chopek, M.W.; Girma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.
 Biochemistry 25, 3146-3155, 1986
 A/Title: Human von Willebrand factor: a multivalent protein composed of identical subunit
 A/Reference number: A23464; MUID:86269892; PMID:3015199
 A/Accession: A23464
 A/Molecule type: protein
 A/Residues: 764-773, 2803-2813 <CHO>
 A/Cross-references: UNIPARC:UPI0000174323; UNIPARC:UPI0000174324
 R/Dent, J.A.; Berkowitz, S.D.; Ware, J.; Kaasper, C.K.; Ruggeri, Z.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990
 A/Title: Identification of a cleavage site directing the immunohistochemical detection of mole
 A/Reference number: A36013; MUID:90349604; PMID:2385594
 A/Accession: A36013
 A/Molecule type: protein
 A/Residues: 1606-1617 <DEN>
 A/Cross-references: UNIPARC:UPI0000174325
 R/Fey, P.U.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B.M.;
 Science 233, 995-998, 1986
 A/Title: Propylpeptide of von Willebrand factor circulates in blood and is identical to
 A/Reference number: A60913; MUID:86208144; PMID:3486471
 A/Accession: A60913
 A/Molecule type: protein
 A/Residues: 576-590 <FAY>
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 A/Gene: GDB:WVF
 A/Cross-references: GDB:119125; OMIM:193400
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 C/Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicat
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 F:23-763/Product: von Willebrand antigen II #status predicted <WA1>
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 F:387-745/Domain: type D repeat 2 <DD2>
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 F:784-865/Domain: D' <DDD>
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 F:836-853, 2400-2515, 2544-2662/Region: duplication
 F:842-1130, 1934-2203/Region: duplication
 F:866-1241/Domain: type D repeat 3 <DD3>
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 F:1496-1654/Domain: von Willebrand factor type A repeat homology <VWA2>
 F:1689-1854/Domain: von Willebrand factor type A repeat homology <VWA3>
 F:1947-2295/Domain: type D repeat 4 <DD4>
 F:2296-2330/Domain: type B repeat 1 <VB1>

F:2340-2365/Domain: type B repeat 2 <VB2>
F:2375-2399/Domain: type B repeat 3 <VB3>
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F:2507-2509/Region: cell attachment (R-G-D) motif
F:2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>
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F:1147/Binding site: carbohydrate (asn) (covalent) #status atypical
F:1248,1255,1256,1468,1477,1487,1679,2298/Binding site: carbohydrate (Thr) (covalent) #
F:1263,1486/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 7.6%; Score 266; DB 1; Length 2813;

Best Local Similarity 21.9%; Pred. No. 6.7e-09;

Matches 102; Conservative 85; Mismatches 200; Indels 78; Gaps 19;

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QY 368 G-LSNVGRAISFVTKNFSPKANGNSGAPNVVVVWDGMPYDKVEASRLAESGINIF 426
Db 1352 SQVASTSEVLKYTLFQIFSKI--DRPEASRIALLMAS-----QEPQMSRN-----FV 1398
QY 427 ITIEGAANEKQYVEP-----NFANKAVCRCTNGPFYSLHYOSWFGIHKTIQPL 474
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Search completed: June 7, 2006, 01:19:55

Job time : 47 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2006, 01:31:57 ; Search time 16 Seconds
(without alignments)
490.073 Million cell updates/sec

Title: US-10-063-540-34

Perfect score: 3502
Sequence: 1 MRRVLTMRKASVIEMLVL.....QYVPRITQICTEFPNQPRN 678

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA New*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|---------------------|-------------------|
| 1 | 3502 | 100.0 | 678 | US-10-196-749-150 | Sequence 150, App |
| 2 | 3502 | 100.0 | 678 | US-11-101-316-34 | Sequence 34, Appl |
| 3 | 1129.5 | 32.3 | 550 | US-10-196-749-46 | Sequence 46, Appl |
| 4 | 232 | 6.6 | 180 | US-09-970-076-3 | Sequence 3, Appl |
| 5 | 231 | 6.6 | 1152 | US-10-511-937-2444 | Sequence 2444, Ap |
| 6 | 204.5 | 5.8 | 436 | US-10-505-928-592 | Sequence 592, App |
| 7 | 203.5 | 5.8 | 1170 | US-10-511-937-3007 | Sequence 3007, Ap |
| 8 | 193 | 5.5 | 1151 | US-11-246-999-103 | Sequence 103, App |
| 9 | 192.5 | 5.5 | 1034 | US-11-246-999-43 | Sequence 43, Appl |
| 10 | 192.5 | 5.5 | 1189 | US-11-246-999-35 | Sequence 35, Appl |
| 11 | 190.5 | 5.4 | 437 | US-11-293-697-3386 | Sequence 3386, Ap |
| 12 | 170.5 | 4.9 | 198 | US-10-196-749-70 | Sequence 70, Appl |
| 13 | 143.5 | 4.1 | 500 | US-10-196-749-70 | Sequence 4, Appl |
| 14 | 133.5 | 3.8 | 524 | US-11-293-697-3442 | Sequence 3442, Ap |
| 15 | 131.5 | 3.8 | 247 | US-11-330-353-4 | Sequence 4, Appl |
| 16 | 113.5 | 3.2 | 405 | US-10-953-349-1810 | Sequence 1810, Ap |
| 17 | 113.5 | 3.2 | 413 | US-10-953-349-1809 | Sequence 1809, Ap |
| 18 | 113.5 | 3.2 | 422 | US-10-953-349-1808 | Sequence 1808, Ap |
| 19 | 112 | 3.2 | 231 | US-11-293-697-4167 | Sequence 4167, Ap |
| 20 | 111.5 | 3.2 | 382 | US-10-953-349-24980 | Sequence 24980, A |
| 21 | 110 | 3.1 | 338 | US-10-953-349-5351 | Sequence 5351, Ap |
| 22 | 110 | 3.1 | 352 | US-10-953-349-5350 | Sequence 5350, Ap |
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| 24 | 108 | 3.1 | 422 | US-10-953-349-26025 | Sequence 26025, A |
| 25 | 107 | 3.1 | 880 | US-10-953-349-6391 | Sequence 6391, Ap |

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| 27 | 103.5 | 3.0 | 577 | US-11-293-697-3929 | Sequence 3929, Ap |
| 28 | 103 | 2.9 | 334 | US-11-293-697-2527 | Sequence 2527, Ap |
| 29 | 102 | 2.9 | 409 | US-10-953-349-32547 | Sequence 32547, A |
| 30 | 102 | 2.9 | 652 | US-10-953-349-5551 | Sequence 5551, Ap |
| 31 | 102 | 2.9 | 693 | US-11-293-697-3849 | Sequence 3849, Ap |
| 32 | 101 | 2.9 | 326 | US-10-953-349-17338 | Sequence 17338, A |
| 33 | 101 | 2.9 | 343 | US-10-953-349-17337 | Sequence 17337, A |
| 34 | 101 | 2.9 | 350 | US-10-953-349-17336 | Sequence 17336, A |
| 35 | 100.5 | 2.9 | 314 | US-11-293-697-2665 | Sequence 2665, Ap |
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| 37 | 100 | 2.9 | 333 | US-09-970-076-8 | Sequence 8, Appl |
| 38 | 100 | 2.9 | 368 | US-09-970-076-2 | Sequence 2, Appl |
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| 42 | 99 | 2.8 | 338 | US-10-953-349-24981 | Sequence 24981, A |
| 43 | 99 | 2.8 | 384 | US-10-505-928-395 | Sequence 395, App |
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ALIGNMENTS

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RESULT 1
US-10-196-749-150
Sequence 150, Application US/10196749
Publication No. US200609486441
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhen
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196, 749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 150
LENGTH: 678
TYPE: PRT
ORGANISM: Homo Sapien
US-10-196-749-150

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Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 4,3e-235;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-11-101-316-34
; Sequence 34, Application US/11101316
; Publication No. US2006009657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 34
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-34

Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 4,3e-235;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 661 VPRIIQNICTEFNSQPRN 678
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; Sequence 46, Application US/10196749
; Publication No. US2006009486A1
; GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zheng, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 46
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-196-749-46

Query Match      32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 5.4e-71;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

QY 44 INCDVKAAGKITDPFIYKCPAGCDPKYHVYGTDVYASYSVCGAAVHSGVLDNSGGKITL 103
DB 32 ITCTRTGIDIRKEKADVLCFPGGCPLEERSYVGNIVYASVSSICGAAYHKGVIASNSGGFVR 91
QY 104 VRKVAAGSGYKGSYNGVOSLSLPWRRESFVLESKPKKGYTPBALTYSSKSPAAQAG 163
DB 92 VYSLPGRENYSVVDANGIOSQMLSRMSASFTYTKGK-----SSTQEKATGA- 137
QY 164 ETTAAVQRPPIPGTTAQPVTLMQLAVVAATPTTLRPSBSAATSTISIRPQSVGHR 223
DB 138 -----VSTAH----- 143
QY 224 QEMDLMSTATYTSQNRPRADPGIORODPSGAAPQKPGADVSLGLVPEKEELSTQSLBPV 283
DB 144 -----PTGKRLKK-----TPKK----- 156
QY 284 SLGDPNCKIDISFLIDGSTSGKRRFRIQKQLADVAQALDIGPAPLMGVVQGDNDPAT 343
DB 157 -TGKNDCKADIAPLIDGSFNIGORRFNIOKNFVGKVALMLGIGTEGPHVGLVQASEHPKI 215
QY 344 HFNKTHNSRDLKATAEKTIQORGLSNVGRALISVTGNFSPKANGNSGAPNVVVVWD 403
DB 216 EFYIKNFTSADVFAIKVEGFRGNSNTGALKTKHTAKPFTVDAGVKRGIPKVVVVVID 275
QY 404 GMPDKEVEASRLARESGINIFITIEGAENEEKQYVVEPRFANKAVCRITNGFYSLAVOS 463
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DB 276 GMPSDDIEEAGIVAREFVNFIIVSAKPIDEELGMVDVTFVVKAYCERNNGFFPSYHMPN 335
QY 464 WFGHLKTLQPLVXKVCOTDRDLACGKTCUNSDIGVIDGSSVGVNGNRTYLOFNTLTK 523
DB 336 WFGTKYKVPLOVQKCTHEOQMSCKTCYNSVNIAPFLIDGSSVGDNSRMLHLEFVSNIAK 395
QY 524 EFEISDTRIGAQVYTYEORLEFGFDKSSKPDILNAIKRVGWSGGSTGAALNFALE 583
DB 396 TFEISDIGAKIAAQQFTYDQRTSFSDYSIKENLAVIRNIRYMSGGTATGDALSTFVR 455
QY 584 QLEK-KSKPNKRLMLITDGRSYDVRITPAAAHKGVITTYALGVMAAOELEVAT 641
DB 456 NVFPIRESPMK-NFLVIVTDGQSYDDYQGPAAAHADAGITIFSVGAMAPLDDLKOMAS 514
QY 642 HPARDHSFVDEPDNLHQVPRITQNTCTEF 672
DB 515 KPESHAFTRFETGLEPIVSDVIRGICRDP 545

RESULT 4
US-09-970-076-3
; Sequence 3, Application US/09970076
; Publication No. US20060110801A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/09/970,076
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: von Willebrand
; US-09-970-076-3

Query Match      6.6%; Score 232; DB 1; Length 180;
Best Local Similarity 32.0%; Pred. No. 1.5e-09;
Matches 48; Conservative 38; Mismatches 60; Indels 4; Gaps 2;

QY 292 IDLSFLIDGSTSGKRRFRIQKQLADVAQALDIGPAPLMGVVQGDNDPATHTLTKHT 351
DB 2 LDVVFLLDSSGSGWGNRRELKAEFLVCLKVLEOLDIGPRDRGLVTFSSDAVLEPLNDQ 61
QY 352 NSRDLKTAIEKIT-QRGGLSNVGRALISFTGNFSPKANGNSGAPNVVVVWDGMPDVKV 410
DB 62 SKDMLLEMLANLSTSLGGTTLGAALEALENLSEBSAGSRGAPKVLILITDGSNDGG 121
QY 411 EASRLARE--SGINIFITIEGAENEEK 437
DB 122 EDILKAKEKRLKRSQVVFVVGNAVDEEE 151

RESULT 5
US-10-511-937-2444
; Sequence 2444, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
```

```

; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2444
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2444
```

Query Match 6.6%; Score 231; DB 6; Length 1152;

Best Local Similarity 33.0%; Pred. No. 2.5e-08;

Matches 62; Conservative 39; Mismatches 63; Indels 24; Gaps 7;

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QY 494 ADIGFVIDSSVGTGNFRTVLOFVNLTKFEISDTRIGAVQYTEORLEFGPKYS 553
DB 149 SDIAFLIDGSGSITPHDFRMRKEFVSTVME--QLKSKTTLFLMQLSEEFHHTTFEFQ 206
QY 554 SKPDILNAIKRVGWSGSGTGAALNPALEQLF--KKSXPKRKLMLITDGR----- 604
DB 207 NNPNRSLVPIPTQLGRTHTATGIRKVRRLFNITGARNAPKILVITDGRKFGDPL 266
QY 605 SYDDVRTPMAAHLKGVITTAIGVAAA-----AOEEVLATHPARDHSFVDFEDNLHQ 659
DB 267 GYEDV-IP--EADREGVIRVYIGVADAFRSEKSRQELNTASKPRDHVFQVNNFEAL-- 321
QY 660 YVPRION 667
DB 322 ----KTION 326
```

RESULT 6

```

; Sequence 592, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 592
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-592
```

Query Match 5.8%; Score 204.5; DB 6; Length 436;

Best Local Similarity 22.0%; Pred. No. 4.2e-07;

Matches 95; Conservative 70; Mismatches 193; Indels 73; Gaps 18;

```

QY 290 CK--IDLSFLIDSGTSGKRRFRIQKQLADVAQALD-----IGPAGPLMGVVOYGDN 340
DB 17 CKGGPDLFLVLDSSBSISIGLQNFELADFPVKVIDRLSRDELVKFEFGGSGVAGVVOY--- 73
QY 341 PAFHFNLIKHTF-----NSRDLKTAIEKTIORGKLSNVGRAISFVTKQFFSKANGNRS 392
DB 341 PAFHFNLIKHTF-----NSRDLKTAIEKTIORGKLSNVGRAISFVTKQFFSKANGNRS 392
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DB 74 --SHSQWQEHVLSRSPSIRNVQELKEAIKSLQWMAAGTFTGEALQYTRDQLLPSPNNR- 130
QY 393 GAPVVVVWVDG-WPTKXVEASRLAESGINIFETIEGAAB-----NEKQYVVE----- 442
DB 131 ----IAVITDGSSTDRDTPPLANVCSPGIQVSVGIKVFDFIPSSDQNLNYSQGLA 186
QY 443 PNFANKAVCRNTEGFSYSLHVSFGLAKTLOPLVKRVCDTRLACSKTCLNSADIGFVIDG 502
DB 187 PSQGRPGLSLVKENYVABLLDADFUKNTVAGICIDKKCPD--YTCPIFFSSPADITILLP 244
QY 503 SSSVGTGNFRTVLOFVNLTKFEISDT-----DTRIGAVQY--TYEOR-----LBERFD 550
DB 245 PPDVGSNPFDTTKRFARLAEFLTAGRTDPADVRAVAVQYSGTGQQRPERASLQF-LQ 303
QY 551 KYSKPDILNAIKRVGWSGSGTGAALNPALEQLF--KKSXPKRKLMLITDGRSYD--- 607
DB 304 NYTR--LASAVDAMPINATDVNDALGVYTFYREASGGAKKRLLLSDNSQCATP 360
QY 608 -DVRIPMAAHLKGVITTAIGVAAAQE-ELEVIAITHPARD-----HSFVDFEDNL 657
DB 361 AAIEKAVQEAQRAGIEIFVVVVGQVNEPHIRVLVTGKTAEDVAVAGESHLFRVPSYQAL 420
QY 658 ----HQYPR 663
DB 421 LRGVFHQTVSR 431
```

RESULT 7

```

US-10-511-937-3007
; Sequence 3007, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Kohlgenmuh, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3007
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-3007
```

Query Match 5.8%; Score 203.5; DB 6; Length 1170;

Best Local Similarity 23.8%; Pred. No. 2e-06;

Matches 85; Conservative 57; Mismatches 124; Indels 91; Gaps 14;

```

QY 383 FFSKAN-----GNRSGAP-----NVVVVVWVDGWPDKVEASRLARES 420
DB 19 FFAPASSYINDVANGASFSPPRAGRHPGRVLOVAGKVIY--GAGEGSGTSGSLVQCOS 75
QY 421 GI-NIFPITTEGAENEKQYVNEPNFANKAVCRNTEGFSYSLHVSFGLAKTLOPLVKRV 479
DB 76 GTGHCUPVTLRGS-----NYTSKYLGMT-----LATPPTDSIIACDPGLSRTC 119
QY 480 DTD-----RLACSKTCLNSADIGVINGSSSVGTGNFRTVLOFV 518
DB 480 DTD-----RLACSKTCLNSADIGVINGSSSVGTGNFRTVLOFV 518
```

Dh 120 DONTYSLCYLFRNLOGPMLOGRPFGEQCKGNVDVLFEDGMSLQDPDEFOKILDFM 179
Qy 519 TNLTFEPISDTRIGAVOYTYEORLEFGFDKYS--SKPDILNAIKRGVWSSGTSTGA 576
Dh 180 KDVK--KLSTSTQFAAVQSTSKYTFDFSDYKMKDPDL--LKVKHMLLTNTFG 235
Qy 577 AINFALEQLFKK--SKPNRKLMLITDGRSYDVRIPAMAHLKGVITTAIGV----- 628
Dh 236 AINVAATEVFREELGARDATKVLIIITDGEATDSCNIDA-----AKDIIRYITIGIKHFQ 291
Qy 629 AMAAOEELVATHPARHSEFFVDFDMLHOYVPIITONI-----CTEFSQ 675
Dh 292 TKESQETLHKRASKPASEFVXILDTFEKLKDLFTLEQKIVIEGTSKODLTSFME 348

RESULT 8
US-11-246-999-103
; Sequence 103, Application US/11246999
; Publication No. US20060099622a1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-246-999-103

Query Match 5.5%, Score 193; DB 7; Length 1151;

Best Local Similarity 20.7%, Pred. No. 1,1e-05;
Matches 84; Conservative 59; Mismatches 134; Indels 128; Gaps 13;

Qy 269 LVPKEELSTQSLPEVSLDLPNCKIDLSFLIDGSTSIGRRFRIOQLADVAQALDIPGA 328
Dh 133 IAPVQEGSTQ-----LDIVIVLDGSNSI--YPMDSVAFALNDLKKRMDIPK 177
Qy 329 GPLMGVVOYGDNPATHTNLKTHNSRDKTAIEKTORGSLSNV--GRAISFVTKNFSKA 387
Dh 178 QTVGIYOYGENVTHFEFLNKYSTEEVLVAAKIVQCGROTALGTARKEAFTEA 237
Qy 388 NGRSGAPNVVWVDGWPDT--KVEASRLARESGINIFITTEGA-----AE 434
Dh 238 RGAARGVAKVAVITVDGSHNHLKVKYIQCEDENIQRFISALIGSYNRGNLSTEKFE 297
Qy 435 NEKOYVPE--NFANKAVCRITNGFYSLHVOSEFGLHTLOPLVRCVCDTRLACSKTCL 491
Dh 298 EINSIAEPEKHFNF-----VSDELALVITVITLGRIT----- 331
Qy 492 NSADIGVIVDSSSVGTGNFRTVLOFTNLTKFEFISDTRIGAVOYTYEORLEFGDK 551
Dh 332 -----FALBATADQSAASF-----EMEMSQT-----GRSA 356
Qy 552 YSSKPDILNAIKRGVWSSGTSTGA-----INFALAEQLFKSKRKNKKMLILIDG 603
Dh 357 HYSODWMLGAVGAVDMNGTVVMOKASQIILPRNTTFVEST--KKNP----- 403

Qy 604 RSYDDVRIPAMAHLKGVITTAIGVAMAAOELEVIATHPARDS 648
Dh 404 -----LASLYGYTVNSATASGSDVLYIAGQPRVNH 434

RESULT 9
US-11-246-999-43
; Sequence 43, Application US/11246999
; Publication No. US20060099622a1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-246-999-43

Query Match 5.5%, Score 192.5; DB 7; Length 1034;
Best Local Similarity 30.1%, Pred. No. 9.8e-06;
Matches 65; Conservative 31; Mismatches 89; Indels 31; Gaps 8;

Qy 453 TNGFYSLHVOSEFGLHTLOPLVRCVCDTRLACSKTCLNSADIGFVIDSSSVGTGNFR 512
Dh 135 TTGMCS--RVNSNFRPSKVAALQR-----CQTYMDIVIVLDGSNSIYP--WV 179
Qy 513 TVLOFTNLTKFEFISDTRIGAVOYTYEORLEFGFDKYSKPDILNAIKRGVWSSGT 572
Dh 180 EVGHFLINILKKFTYIGRQIQVGVYGEDVHFEFLNDYSVDVVAASHIQ--RGCT 238
Qy 573 STGAA--INFALAEQLFKK--SKPNRKLMLITDGRSYD--DVRIPAMAHLKGVITTAIG 627
Dh 239 ERTTAFGIEFARSAFQGRKAKKVMIVITDGSHTSPLEKVIQOSERDNTTRYAVA 298
Qy 628 VAW-----AAOELEVIATHPARHSEFFVDE 653
Dh 299 VLGYYNRGINPETFLNEIKYIASDPDKHFENVTD 334

RESULT 10
US-11-246-999-35
; Sequence 35, Application US/11246999
; Publication No. US20060099622a1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407

;; PRIOR FILING DATE: 2000-04-19
;; PRIOR APPLICATION NUMBER: PCT/US99/25031
;; PRIOR FILING DATE: 1999-10-27
;; PRIOR APPLICATION NUMBER: 60/105,971
;; PRIOR FILING DATE: 1998-10-28
;; NUMBER OF SEQ ID NOS: 149
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 35
;; LENGTH: 1189
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-246-999-35

Query Match 5.5%; Score 192.5; DB 7; Length 1189;
Best Local Similarity 30.1%; Pred. No. 1.2e-05;
Matches 65; Conservative 31; Mismatches 89; Indels 31; Gaps 8;

QY 453 TNGFYSLHVQSWFGMLHTLQPLVYKVCDDTLRLACSKTCLNSADIGFYIDSSSVGTGNFR 512
DB 135 TTGMCS-RVNSNFRFSKTVAPALQR-----CQFYMDIVIVLDGNSIYP--WV 179
QY 513 TVLQPTNLTKPEPISDTDRIGAVQYTYEQRLEFGFDKYSKRDILNAIKRVGWSGCT 572
DB 180 EVQHFLNLIKKEYIGGQIQVGVOYGEDVHFFHLNDRSVKDVVEASHIQ-RGGT 238
QY 573 STGAA--INFALBOLFCK-SKPNRKLMLITDGRSYD--DVRIPAMAHLKGVITYAIG 627
DB 239 ETTTAFGEIETAFARSAPFGKGRKAKKMYITTDGESHSDPLEKVIQGSSENDVTRAYVA 298
QY 628 VAM-----AAOELEVIATHPARHSFFVDE 653
DB 299 VLGYYNRGINPETFLNEIKYIASDPDDKHFENVTD 334

RESULT 11
US-11-293-697-3386
;; Sequence 3386, Application US/11293697
;; Publication No. US20060105376A1
;; GENERAL INFORMATION:
;; APPLICANT: HELIX RESEARCH INSTITUTE
;; TITLE OF INVENTION: Novel full length cDNA
;; FILE REFERENCE: H1-A0106
;; CURRENT APPLICATION NUMBER: US/11/293,697
;; CURRENT FILING DATE: 2005-12-05
;; PRIOR APPLICATION NUMBER: US/10/108,260
;; PRIOR FILING DATE: 2002-03-28
;; NUMBER OF SEQ ID NOS: 5458
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3386
;; LENGTH: 437
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-293-697-3386

Query Match 5.4%; Score 190.5; DB 7; Length 437;
Best Local Similarity 30.1%; Pred. No. 3.9e-06;
Matches 65; Conservative 30; Mismatches 90; Indels 31; Gaps 8;

QY 453 TNGFYSLHVQSWFGMLHTLQPLVYKVCDDTLRLACSKTCLNSADIGFYIDSSSVGTGNFR 512
DB 135 TTGMCS-RVNSNFRFSKTVAPALQR-----CQFYMDIVIVLDGNSIYP--WV 179
QY 513 TVLQPTNLTKPEPISDTDRIGAVQYTYEQRLEFGFDKYSKRDILNAIKRVGWSGCT 572
DB 180 EVQHFLNLIKKEYIGGQIQVGVOYGEDVHFFHLNDRSVKDVVEASHIQ-RGGT 238
QY 573 STGAA--INFALBOLFCK-SKPNRKLMLITDGRSYD--DVRIPAMAHLKGVITYAIG 627
DB 239 ETTTAFGEIETAFARSAPFGKGRKAKKMYITTDGESHSDPLEKVIQGSSENDVTRAYVA 298
QY 628 VAM-----AAOELEVIATHPARHSFFVDE 653
DB 299 VLGYYNRGINPETFLNEIKYIASDPDDKHFENVTD 334

RESULT 12
US-09-970-076-4
;; Sequence 4, Application US/09970076
;; Publication No. US20060110801A1
;; GENERAL INFORMATION:
;; APPLICANT: Young, John A.T.
;; APPLICANT: Bradley, Kenneth A.
;; APPLICANT: Collier, Robert J.
;; APPLICANT: Mogridge, Jeremy S.
;; TITLE OF INVENTION: Antitoxin Receptor
;; FILE REFERENCE: 960296,97745
;; CURRENT APPLICATION NUMBER: US/09/970,076
;; CURRENT FILING DATE: 2001-10-03
;; PRIOR APPLICATION NUMBER: 60/251,481
;; PRIOR FILING DATE: 2000-12-05
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 198
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-970-076-4

Query Match 4.9%; Score 170.5; DB 1; Length 198;
Best Local Similarity 36.8%; Pred. No. 3e-05;
Matches 42; Conservative 18; Mismatches 51; Indels 3; Gaps 2;

QY 292 IDSFLIDGSTSGKRRFRQKQLADVAQALDIGRGLMGVGVGDNPATHTNLKTHT 351
DB 5 IDVVVVCDESNST--YPMWDAVKNLEKFFVQGLDIGTKTQVGILQYANNRVVENLNTYK 62
QY 352 NSRDLKTAIEKTRQGRG-LSNVGRAISFVTKNFSKANGRSAGPNNVVVVMDG 404
DB 63 TKESMTVATSQTSQYGEDLTNTFGALQYARKKXYSAGGRSAATKVMVVTDG 116

RESULT 13
US-10-196-749-70
;; Sequence 70, Application US/10196749
;; Publication No. US20060094864A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gueney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3430R1C340
;; CURRENT APPLICATION NUMBER: US/10/196,749
;; CURRENT FILING DATE: 2002-07-16
;; PRIOR APPLICATION NUMBER: 10/052586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21

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; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See file wrapper or PALM.
; SEQ ID NO 70
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-70

Query Match          4.1%; Score 143.5; DB 6; Length 500;
Best Local Similarity 34.9%; Pred. No. 0.0085;
Matches 38; Conservative 15; Mismatches 43; Indels 13; Gaps 4;

QY 29 ETAKKIRKPKFTVPOINCDVAKGIID-----PEFIVKCPAGCQ--DPKY-HVYGTG 77
DB 379 QSANSTFVSKVTQAVTCETVEQLCPHPKASHCPR--VYCPNQCWQANPHYARVIGTR 436
QY 78 VYASYSVCCAAHSGVLDSGGKILVRKAVAGSGYKGSYNGVQSL 126
DB 437 VYSDLSISICRAAHVAGVNRHNGYDVPVDRKTYIASFONGIFSESL 485

RESULT 14
US-11-293-697-3442
; Sequence 3442, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NOVEL full length CDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3442
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3442

Query Match          3.8%; Score 133.5; DB 7; Length 524;
Best Local Similarity 38.6%; Pred. No. 0.045;
Matches 32; Conservative 14; Mismatches 34; Indels 3; Gaps 2;

QY 44 INCDVAKGIIDPEFIVKCPAGCQDPKYHYVG--TDVYASYSVCCAAHSGVL-DNSGG 100
DB 156 ITCERASHYKTYSKFCPCAGCRDVAAGDISGMVWDGYRDTSLCKAIIHAGIADDELGG 215
QY 101 KILVRKAVAGSGYKGSYNGVQSL 123
DB 216 QISVLQRKGISRYEGIIANGVLS 238

RESULT 15
US-11-330-353-4
; Sequence 4, Application US/11330353
; Publication No. US20060105429A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
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; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/330,353
; FILING DATE: 12-Jan-2006
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,624
; FILING DATE: 10-Sep-2002
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-Jan-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-Jul-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-Jan-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-Jan-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith P.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-330-353-4

Query Match          3.8%; Score 131.5; DB 7; Length 247;
Best Local Similarity 23.3%; Pred. No. 0.021;
Matches 44; Conservative 34; Mismatches 100; Indels 11; Gaps 6;

QY 490 CINSADIGFVIDSSSVGTGNFRVLQFVNLTKFEISDTDRIGAVQYTYEQRLEGF 549
DB 43 CSRLLDLVFLDDSSSRLESEAEFVLKAFVYDMERLRIQKWRVAVAVEYHDSHAYIGL 102
QY 550 DKYSKPDILNAIKRVGWSGG--TSTGAALNPLBQLFK-SKPNRKMLITLTDGR-- 604
DB 103 -KDRKRPSRLRIASQVYAGSQVASTSEVLYKTLFOIFS KIDRPEASRIALLMASQEP 161
QY 605 ---SYDVRIPMAAHKGVITTAIGVA--MAAOELEVIAHTPARDSFPVDEFDNIHQY 660
DB 162 QRMSRNFPVRY-VQGLKKKKVIVIPVIGIPHANLKQIRLIEKQAPENKAFVLSVDELEQ 220
QY 661 VPRITONIC 669
DB 221 RDEIVSYLC 229

Search completed: June 7, 2006, 01:35:10
Job time : 18 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 7, 2006, 01:38:52 ; Search time 44 Seconds
(without alignments)
1482.613 Million cell updates/sec

Title: US-10-063-540-34

Perfect score: 678
Sequence: 1 MRTVVLTKASVIEMLVL.....QVPRITQICTEFNQPRN 678

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 3175

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR_80:.*
2: pir1:.*
3: pir2:.*
4: pir3:.*
5: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Query Length | DB ID | Description |
|------------|-------|-------------|--------------|----------|--------------------|
| 1 | 8 | 1.2 | 174 | 2 D87197 | conserved hypotet |
| 2 | 8 | 1.2 | 230 | 2 H95040 | hypothetical prote |
| 3 | 8 | 1.2 | 323 | 1 H64130 | glycosyl transfera |
| 4 | 8 | 1.2 | 359 | 2 T44816 | btp protein (impor |
| 5 | 8 | 1.2 | 368 | 2 F84300 | bacteriorhodopsin |
| 6 | 8 | 1.2 | 394 | 2 A97244 | moaA/NirX family F |
| 7 | 8 | 1.2 | 400 | 1 J00756 | nicotinate phospho |
| 8 | 8 | 1.2 | 400 | 2 F90755 | nicotinate phospho |
| 9 | 8 | 1.2 | 400 | 2 D85619 | nicotinate phospho |
| 10 | 8 | 1.2 | 452 | 2 AG1223 | cobyrinic acid a,c |
| 11 | 8 | 1.2 | 695 | 2 C86731 | copper-potassium t |
| 12 | 8 | 1.2 | 1464 | 2 T13716 | baobab gene prote |
| 13 | 7 | 1.0 | 40 | 2 S08656 | protein VI - human |
| 14 | 7 | 1.0 | 45 | 2 A45700 | envelope glycoprot |
| 15 | 7 | 1.0 | 96 | 2 T11096 | NMDH2 dehydrogenas |
| 16 | 7 | 1.0 | 107 | 2 T19221 | hypothetical prote |
| 17 | 7 | 1.0 | 115 | 2 S38715 | ig kappa chain V r |
| 18 | 7 | 1.0 | 129 | 2 B64510 | hypothetical prote |
| 19 | 7 | 1.0 | 131 | 2 C82462 | hypothetical prote |
| 20 | 7 | 1.0 | 137 | 2 T06380 | histone H2B-3 - to |
| 21 | 7 | 1.0 | 141 | 2 T48925 | ribosomal L1 prote |
| 22 | 7 | 1.0 | 147 | 2 T09722 | histone H2B1 - upl |
| 23 | 7 | 1.0 | 152 | 2 S48838 | histone H2B - gard |
| 24 | 7 | 1.0 | 153 | 2 F95336 | hypothetical prote |
| 25 | 7 | 1.0 | 156 | 1 GNVOI2 | genome-linked prot |
| 26 | 7 | 1.0 | 156 | 1 GNVOI2 | genome-linked prot |
| 27 | 7 | 1.0 | 156 | 1 GNVOI2 | genome-linked prot |
| 28 | 7 | 1.0 | 172 | 2 F84383 | hypothetical prote |
| 29 | 7 | 1.0 | 172 | 2 C64400 | hypothetical prote |

| | | | | | |
|----|---|-----|-----|----------|--------------------|
| 30 | 7 | 1.0 | 177 | 2 G64071 | H--transporting tw |
| 31 | 7 | 1.0 | 217 | 1 JS0630 | formate dehydrogen |
| 32 | 7 | 1.0 | 217 | 2 H90888 | formate dehydrogen |
| 33 | 7 | 1.0 | 217 | 2 A85729 | formate dehydrogen |
| 34 | 7 | 1.0 | 235 | 2 A36941 | phosphoribosylamin |
| 35 | 7 | 1.0 | 235 | 2 H95004 | hypothetical prote |
| 36 | 7 | 1.0 | 236 | 1 A30225 | regulatory protein |
| 37 | 7 | 1.0 | 236 | 2 T51073 | regulatory protein |
| 38 | 7 | 1.0 | 243 | 2 H95282 | probable lysR-type |
| 39 | 7 | 1.0 | 249 | 2 E97877 | phosphoribosylamin |
| 40 | 7 | 1.0 | 255 | 2 AD2307 | hypothetical prote |
| 41 | 7 | 1.0 | 257 | 2 G70581 | hypothetical prote |
| 42 | 7 | 1.0 | 258 | 2 UQ1666 | transcription init |
| 43 | 7 | 1.0 | 261 | 2 C72488 | probable indole-3- |
| 44 | 7 | 1.0 | 267 | 2 AB1280 | probable sigma fac |
| 45 | 7 | 1.0 | 268 | 2 B75279 | survival protein S |

ALIGNMENTS

```

RESULT 1
D87197 conserved hypothetical protein ML2304 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 31-Dec-2004
C:Accession: D87197
R:Coile, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Dutnoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86309; MUID:21128732; PMID:11234002
A:Accession: D87197
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-174 <STO>
A:Cross-references: UNIPROT:Q9CB89; UNIPARC:UPI00000C6B68; GB:AL450380; NID:g13093929; P
A:Gene: ML2304
C:Superfamily: translation initiation inhibitor, TracF type

Query Match 1.2%; Score 8; DB 2; Length 174;
Best Local Similarity 100.0%; Pred.No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 VGADVSIG 268
Db 76 VGADVSIG 83

RESULT 2
H95040 hypothetical protein SP0348 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: H95040
R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
son, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,
nson, T.; Hickey, E.R.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: H95040
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <KUR>
A:Cross-references: UNIPROT:Q97S16; UNIPARC:UPI0000128247; GB:AE005672; P1DN:AAK74521.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0348

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C:Superfamily: Streptococcus agalactiae cpsB protein

Query Match 1.2%; Score 8; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 593 KRKLMTLI 600
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DB 20 KRKLMTLI 27

RESULT 3

H64130 glycosyl transferase homolog H1578 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: H64130

R:Plaschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: H64130

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1323 <RIGR>

A:Cross-references: UNIPROT:Q57287; UNIPARC:UPI000013AD7D; GB:U12832; GB:L42023; NID:g15 C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 1.2%; Score 8; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ETAKKIKR 36
|||||
DB 231 ETAKKIKR 238

RESULT 4

T44816 bfp protein [imported] - Halobacterium salinarum

C:Species: Halobacterium salinarum

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T44816

R:Beilach, W.; Friedman, J.; Boyer, H.W.; Pfeiffer, F.

Nucleic Acids Res. 12, 7949-7959, 1984

A:Title: Characterization of a halobacterial gene affecting bacterio-opsin gene expression

A:Reference number: 222850; MUID:85037955; PMID:6093059

A:Accession: T44816

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-359 <BST>

A:Cross-references: UNIPROT:Q47973; UNIPARC:UPI00000628C2; EMBL:X01081; PIDD:CAA25558.1

A:Note: the source is designated as Halobacterium halobium

C:Genetics:

A:Gene: bfp

Query Match 1.2%; Score 8; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 LAVTVAVA 195
|||||
DB 111 LAVTVAVA 118

RESULT 5

F84300 bacteriorhodopsin related protein [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: F84300

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berguet, B.; Pan, M.; Shukla, H.D.; Laeky, S.

; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor

Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: F84300

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-368 <STO>

A:Cross-references: UNIPROT:Q9HPU7; UNIPARC:UPI00000638C9; GB:AE004437; NID:g10580962, P]

C:Genetics:

A:Gene: bfp

Query Match 1.2%; Score 8; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 LAVTVAVA 195
|||||
DB 120 LAVTVAVA 127

RESULT 6

A97244 moa/NirX family Fe-S oxidoreductase CAC2796 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C:Accession: A97244

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: A97244

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <KUR>

A:Cross-references: UNIPROT:Q97FE4; UNIPARC:UPI000006CA635; GB:AE001437; PIDD:AAK80740.1;

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC2796

Query Match 1.2%; Score 8; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 KETAKKIK 35
|||||
DB 125 KETAKKIK 132

RESULT 7

JQ0756 nicotinate phosphoribosyltransferase (EC 2.4.2.11) - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: JQ0756; B64833

R:Wubboldts, M.G.; Terpestra, P.; van Belien, J.B.; Kingma, J.; Meesters, H.A.R.; Witholt,

J. Biol. Chem. 265, 17665-17672, 1990

A:Title: Variation of cofactor levels in Escherichia coli; sequence analysis and express

A:Reference number: JQ0756; MUID:91009224; PMID:2211655

A:Accession: JQ0756

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-400 <WUB>

A:Cross-references: UNIPROT:P18133; UNIPARC:UPI0000168062; GB:J05568; NID:g147306; PIDD:J

A:Experimental source: strain GEC70

R:Blattner, F.R.; Plunkett III, Y.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of *Escherichia coli* K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: B64833
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-400 <BLAT>
A/Cross-references: UNIPARC:UPI0000168062; GB:AE000195; GB:U00096; NID:g1787156; PIDN:AA
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A/Gene: pncB
C/Function:
A/Pathway: nicotinate and nicotinamide metabolism
C/Superfamily: nicotinate phosphoribosyltransferase
C/Keywords: glycosyltransferase; pentosyltransferase

Query Match 1.2%; Score 8; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 ADVAQAALD 324
DB 141 ADVAQAALD 148

RESULT 8
F90755
nicotinate phosphoribosyltransferase [imported] - *Escherichia coli* (strain O157:H7, subsp.
C/Species: *Escherichia coli*
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: F90755
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
A/Reference number: A95629; MUID:21156231; PMID:11258796
A/Accession: F90755
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-400 <NAV>
A/Cross-references: UNIPROT:Q8YDE8; UNIPARC:UPI00001653E6; GB:BA000007; PIDN:BAB34437.1;
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: Ecs1014
C/Superfamily: nicotinate phosphoribosyltransferase

Query Match 1.2%; Score 8; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 ADVAQAALD 324
DB 141 ADVAQAALD 148

RESULT 9
D85619
nicotinate phosphoribosyltransferase [imported] - *Escherichia coli* (strain O157:H7, subsp.
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: D85619
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamotis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: D85619
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-400 <STO>
A/Cross-references: UNIPROT:Q8YDE8; UNIPARC:UPI00001653E6; GB:AE005174; NID:g12514106; F
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: pncB

C/Superfamily: nicotinate phosphoribosyltransferase

Query Match 1.2%; Score 8; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 ADVAQAALD 324
DB 141 ADVAQAALD 148

RESULT 10
AG1223
cobyrrinic acid a,c-diamide synthase homolog *cbiA* [imported] - *Listeria monocytogenes* (str
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AG1223
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Biocker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl, H.
Science 294, 849-852, 2001
A/Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlutener, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A/Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AG1223
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-452 <GLA>
A/Cross-references: UNIPROT:Q8Y7T0; UNIPARC:UPI0000054E4C; GB:NC_003210; PIDN:CAC99269.1
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: *cbiA*
C/Superfamily: cobyrinic acid a,c-diamide synthase

Query Match 1.2%; Score 8; DB 2; Length 452;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 LGVLPKEE 274
DB 191 LGVLPKEE 198

RESULT 11
C86731
copper-potassium transporting ATPase B *copB* [imported] - *Lactococcus lactis* subsp. *lacti*
C/Species: *Lactococcus lactis* subsp. *lactis*
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C/Accession: C86731
R/Bolotin, A.; Winkler, P.; Manger, S.; Jailon, O.; Malarme, K.; Weissenbach, J.; Ehrlich,
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp
A/Reference number: A86625; MUID:21235186; PMID:11137471
A/Accession: C86731
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-695 <STO>
A/Cross-references: UNIPROT:Q9CH87; UNIPARC:UPI0000006919; GB:AE005176; PID:g12723778; PJ
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: *copB*
C/Superfamily: Enterococcus copper-transporting ATPase *copB*; ATPase nucleotide-binding do

Query Match 1.2%; Score 8; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 NKETAKKI 34
DB 540 NKETAKKI 547

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 7, 2006, 01:35:23 ; Search time 304 Seconds

(without alignments)
2063.028 Million cell updates/sec

Title: US-10-063-540-34

Perfect score: 678
Sequence: 1 MRTVLTMKASVIEMLVL.....QYVPRITQICTEFNSQPRN 678

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 6

Total number of hits satisfying chosen parameters: 28349

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Uniprot_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------|
| 1 | 678 | 100.0 | 678 | 2 | Q6UX17_HUMAN |
| 2 | 411 | 60.6 | 693 | 2 | Q9UDN0_HUMAN |
| 3 | 259 | 38.2 | 656 | 2 | Q96DPT_HUMAN |
| 4 | 163 | 24.0 | 203 | 2 | Q6P773_HUMAN |
| 5 | 58 | 8.6 | 650 | 2 | Q3T247_MOUSE |
| 6 | 57 | 8.4 | 652 | 2 | Q3T247_BOVIN |
| 7 | 45 | 6.6 | 628 | 2 | Q8BQ41_MOUSE |
| 8 | 45 | 6.6 | 650 | 2 | Q8BQ41_MOUSE |
| 9 | 45 | 6.6 | 650 | 2 | Q8VH15_MOUSE |
| 10 | 45 | 6.6 | 650 | 2 | Q9C721_MOUSE |
| 11 | 23 | 3.7 | 680 | 2 | Q4RP27_TETNG |
| 12 | 25 | 3.4 | 748 | 2 | Q5NTW9_CHICK |
| 13 | 11 | 1.6 | 553 | 2 | Q8AM56_BRARE |
| 14 | 10 | 1.5 | 1070 | 2 | Q4N1B8_THERP |
| 15 | 10 | 1.5 | 1197 | 2 | Q4URP9_THERP |
| 16 | 9 | 1.3 | 347 | 2 | Q2T7S9_EURTH |
| 17 | 9 | 1.3 | 347 | 2 | Q3JUK5_EURP1 |
| 18 | 9 | 1.3 | 347 | 2 | Q63JB1_BURPS |
| 19 | 9 | 1.3 | 387 | 2 | Q4JVA3_CORYJ |
| 20 | 9 | 1.3 | 560 | 2 | Q4C273_CROWT |
| 21 | 9 | 1.3 | 598 | 2 | Q6G3F2_BARRH |
| 22 | 8 | 1.2 | 63 | 2 | Q4YH15_PLAAB |
| 23 | 8 | 1.2 | 100 | 2 | Q7G2C1_ORYSA |
| 24 | 8 | 1.2 | 106 | 2 | Q4KKH3_PSEFS |
| 25 | 8 | 1.2 | 112 | 2 | Q8G578_BIFLO |
| 26 | 8 | 1.2 | 117 | 2 | Q47M29_THERF |
| 27 | 8 | 1.2 | 124 | 2 | Q480F6_COLP3 |
| 28 | 8 | 1.2 | 155 | 2 | Q7BUZ6_STRPN |
| 29 | 8 | 1.2 | 173 | 2 | Q4SDS4_TETNG |
| 30 | 8 | 1.2 | 174 | 2 | Q9CB89_MYCLE |
| 31 | 8 | 1.2 | 180 | 2 | Q2T220_BURTH |

| | | | | | | |
|----|---|-----|-----|---|----------------|---------------------|
| 32 | 8 | 1.2 | 208 | 2 | Q4UJ42_THERA | Q4UJ42 theileria a |
| 33 | 8 | 1.2 | 208 | 2 | Q2IMW3_RHOA | Q2IMW3 rhodopseuo |
| 34 | 8 | 1.2 | 208 | 2 | Q66166_BRACHA | Q66166 brachydantio |
| 35 | 8 | 1.2 | 208 | 2 | Q90Z99_BRARE | Q90Z99 brachydantio |
| 36 | 8 | 1.2 | 211 | 2 | Q4N6H5_THERP | Q4N6H5 theileria p |
| 37 | 8 | 1.2 | 217 | 2 | Q3GE72_SYTIPHO | Q3GE72 syntrophoma |
| 38 | 8 | 1.2 | 230 | 1 | QPSCL1_STREP | QPSCL1 streptococc |
| 39 | 8 | 1.2 | 230 | 2 | Q54667_STREP | Q54667 streptococc |
| 40 | 8 | 1.2 | 230 | 2 | Q7BV01_STREP | Q7BV01 streptococc |
| 41 | 8 | 1.2 | 230 | 2 | Q8KM01_STREP | Q8KM01 streptococc |
| 42 | 8 | 1.2 | 231 | 2 | Q86887_STREP | Q86887 streptococc |
| 43 | 8 | 1.2 | 231 | 2 | Q371R7_RHOA | Q371R7 rhodopseuo |
| 44 | 8 | 1.2 | 231 | 2 | Q4JYK9_STREP | Q4JYK9 streptococc |
| 45 | 8 | 1.2 | 231 | 2 | Q4JYPO_STREP | Q4JYPO streptococc |

ALIGNMENTS

```
RESULT 1
06UX17_HUMAN PRELIMINARY; PRT; 678 AA.
ID Q6UX17_HUMAN
AC Q6UX17
DT 24-MAY-2005, integrated into UniprotKB/TREMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE VIT.
GN ORFNames=UNO647;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brueh J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Eason D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Kimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R.L., Matanabe C., Mleand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SDPI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
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EMBL: AY358338; AAC88704.1; -; mRNA.
DR HSSP; Q43405; IJBI.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VWA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS00820; LCCL; 1.
DR PROSITE; PS0234; VWF_A; 2.
SQ SEQUENCE 678 AA; 73930 MW; 9870E75A218C686C CRC64;

Query Match 100.0%; Score 678; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTMKASVIEMLVLVTGVHSNKEETAKIKREKFTVPQINCVRKGIITDPEFIV 60
DB 1 MRTVLTMKASVIEMLVLVTGVHSNKEETAKIKREKFTVPQINCVRKGIITDPEFIV 60
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QY 61 KCPAGCDDPKHYVGTVDVYASYSVCGAAVHSGVLNDNSGKILVRKYAGQSGYKGSYNG 120
 DB 61 KCPAGCDDPKHYVGTVDVYASYSVCGAAVHSGVLNDNSGKILVRKYAGQSGYKGSYNG 120
 QY 121 VQSLPRMRESFVLESKPKKGYTPSALTYSSSSKSPAAQAGETTKAYQRPPIGTTAQ 180
 DB 121 VQSLPRMRESFVLESKPKKGYTPSALTYSSSSKSPAAQAGETTKAYQRPPIGTTAQ 180
 QY 181 PVTLMQLLAATVAAATPTTLPSPSPAASSTISIRPOSVGHRSQEMDLMTATYTSSQNR 240
 DB 181 PVTLMQLLAATVAAATPTTLPSPSPAASSTISIRPOSVGHRSQEMDLMTATYTSSQNR 240
 QY 241 PRADPGIQRDPSGAFOKPGADVSLGLVKEELSTQSLPVSIGDPNCKIDSLFILDG 300
 DB 241 PRADPGIQRDPSGAFOKPGADVSLGLVKEELSTQSLPVSIGDPNCKIDSLFILDG 300
 QY 301 STSIGKRRFRIQKQLADVAQALDIGPAGPLMGVVOYGDNPATHPNLKTHNSRDLKTAI 360
 DB 301 STSIGKRRFRIQKQLADVAQALDIGPAGPLMGVVOYGDNPATHPNLKTHNSRDLKTAI 360
 QY 361 EKTTRGGLSNVGRALISFVTKNFSSKANGNSGAPNVVVVWDGPTDKVEASRLARES 420
 DB 361 EKTTRGGLSNVGRALISFVTKNFSSKANGNSGAPNVVVVWDGPTDKVEASRLARES 420
 QY 421 GINIFFTIEGAANEKQYVVEPNFANKAVCRITNGFYSLSHVQSFGLHKTLPVKEVCD 480
 DB 421 GINIFFTIEGAANEKQYVVEPNFANKAVCRITNGFYSLSHVQSFGLHKTLPVKEVCD 480
 QY 481 TDRLACSKTCLNSADIFVIDGSSSVGTGNFRVYLQFVNTLTKEPEISDTRIGAVOYT 540
 DB 481 TDRLACSKTCLNSADIFVIDGSSSVGTGNFRVYLQFVNTLTKEPEISDTRIGAVOYT 540
 QY 541 YEORELEGPQYSSKPIILNAIKRVGWSGTSNGAIPALBQLFKSKPKKMKMILI 600
 DB 541 YEORELEGPQYSSKPIILNAIKRVGWSGTSNGAIPALBQLFKSKPKKMKMILI 600
 QY 601 TDRSRYDVARIIPMAAHLKGVITVTAIGVAAAOEELVIAATHPARDSFFVEDEFNLHOY 660
 DB 601 TDRSRYDVARIIPMAAHLKGVITVTAIGVAAAOEELVIAATHPARDSFFVEDEFNLHOY 660
 QY 661 VPRIIQNICTEFNSQPRN 678
 DB 661 VPRIIQNICTEFNSQPRN 678

RESULT 2
 Q9UDNO_HUMAN PRELIMINARY; PRT; 693 AA.
 ID Q9UDNO_HUMAN Q96DM8;
 AC Q9UDNO; Q96DM8;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 2.
 DT 07-MAR-2006, entry version 26.
 DE Hypothetical protein VIT (Hypothetical protein FLJ32210).
 GN Name=VIT;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Cordes M., Kalicki J., Ames M.;
 RT "The sequence of Homo sapiens BAC clone Rpl1-294111.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura T., Makita H.,
 RA Sekine M., Obaraishi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yaeda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Niimura K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano Y.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiyasu K., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Masegawa K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshihara Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terasima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kakikami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujitaya T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohnori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Matsuura-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegaki T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
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 CC
 DR EMBL: AK056772; BAB1279.1; -; mRNA.
 DR EMBL: AC007363; AAF19243.2; -; Genomic_DNA.
 DR HSSP: O43405; 1JBT.
 DR HGNC: HGNC:12697; VIT.
 DR InterPro: IPR004043; LCCL.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam: PF03815; LCCL; 1.
 DR Pfam: PF00092; VMA; 2.
 DR PRINTS: PR00453; VWFADOMAIN.
 DR SMART: SM00603; LCCL; 1.
 DR SMART: SM00327; VMA; 2.
 DR PROSITE: PS50820; LCCL; 1.
 DR PROSITE: PS50234; VMA; 2.
 KM Hypothetical protein.
 SQ SEQUENCE 693 AA; 75575 MW; 2DE8B2421F2D496D CRC64;

Query Match 60.6%; Score 411; DB 2; Length 693;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 268 GLVKEELSTQSLPVSIGDPNCKIDSLFILDSTSIGKRRFRIQKQLADVAQALDIGP 327
 DB 268 GLVKEELSTQSLPVSIGDPNCKIDSLFILDSTSIGKRRFRIQKQLADVAQALDIGP 342
 QY 328 AGPLMGVVOYGDNPATHPNLKTHNSRDLKTAIEKTTORGLSNVGRALISFVTKNFSSKA 387
 DB 343 AGPLMGVVOYGDNPATHPNLKTHNSRDLKTAIEKTTORGLSNVGRALISFVTKNFSSKA 402
 QY 388 NGRSGAPNVVVVWDGPTDKVEASRLAREGINIFTTIGGAANEKQYVVEPNFAN 447

Db 403 NGNSGAPNVMVWDGWPDTKVEEASRLAESGINIFITIEGAENKQYVVEPNAN 462
Qy 448 KAVRTNGFVSLHVSQWFGHLKHTLOPLVKRCDPDRCLACSTCLNSANIGVIOSSSVG 507
Db 463 KAVRTNGFVSLHVSQWFGHLKHTLOPLVKRCDPDRCLACSTCLNSAIGVIDSSSVG 522
Qy 508 TGNFRTVLOFTNLTKEFEISDTDRIGAVQYVEQRLPEFGDKSKSPDILNAIKRGY 567
Db 523 TGNFRTVLOFTNLTKEFEISDTDRIGAVQYVEQRLPEFGDKSKSPDILNAIKRGY 582
Qy 568 WSGGTSFGAALNPALEBOLFKKSKPNKRKMLITDGRSYDVRIPAMAHLKGVITVAIG 627
Db 583 WSGGTSFGAALNPALEBOLFKKSKPNKRKMLITDGRSYDVRIPAMAHLKGVITVAIG 642
Qy 628 VAMAABELEVIATHPADHSFVDFEFDNLHGVPRRIQNTCTENSGPRN 678
Db 643 VAMAABELEVIATHPADHSFVDFEFDNLHGVPRRIQNTCTENSGPRN 693

RESULT 3

Q96DT1_HUMAN PRELIMINARY; PRT; 656 AA.
ID Q96DT1_HUMAN
AC Q96DT1
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Vitrin.
GN Name=VIT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RA Ren Z.-X., Liu J.G., Mayne R.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL: AF063833; AAL18263.1; -; mRNA.
DR HSSP: O43405; IJBI.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR02035; VWF_A.
DR Pfam: PF03815; LCCL; 1.
DR Pfam: PF00092; VMA; 2.
DR PRINTS: PRO0453; VMPADOMAIN.
DR SMART: SM00603; LCCL; 1.
DR SMART: SM00327; VMA; 2.
DR PROSITE: PS50820; LCCL; 1.
DR PROSITE: PS50234; VMA; 2.
SQ SEQUENCE 656 AA; 71768 MW; E242E0D0FB07CF2C CRC64;

Query March 38.2%; Score 259; DB 2; Length 656;
Best Local Similarity 100.0%; Pred. No. 6e-257;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 420 SGINIFITIEGAENKQYVVEPNANAVCRTNGFVSLHVSQWFGHLKHTLOPLVKRVC 479
Db 398 SGINIFITIEGAENKQYVVEPNANAVCRTNGFVSLHVSQWFGHLKHTLOPLVKRVC 457
Qy 480 DTDPLACSKTCLNSADIGFVIDSSSVGTGNFRVLOFTNLTKEFEISDTDRIGAVQY 539
Db 458 DTDPLACSKTCLNSADIGFVIDSSSVGTGNFRVLOFTNLTKEFEISDTDRIGAVQY 517
Qy 540 TYERLLEGFDPKYSKPDILNAIKRGVWGSSTGALNPALEBOLFKKSKPNKRKMLIT 599
Db 518 TYERLLEGFDPKYSKPDILNAIKRGVWGSSTGALNPALEBOLFKKSKPNKRKMLIT 577
Qy 600 ITDGRSYDVRIPAMAHLKGVITVAIGVAMAABELEVIATHPADHSFVDFEFDNLH 659

Db 578 ITDGRSYDVRIPAMAHLKGVITVAIGVAMAABELEVIATHPADHSFVDFEFDNLH 637
Qy 660 YVPRRIQNTCTENSGPRN 678
Db 638 YVPRRIQNTCTENSGPRN 656

RESULT 4

Q6P7T3_HUMAN PRELIMINARY; PRT; 203 AA.
ID Q6P7T3_HUMAN
AC Q6P7T3
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J.F., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitsuki S., Cavinini P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maita M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL: BC061519; AA61519.1; -; mRNA.
DR InterPro: IPR004043; LCCL.
DR Pfam: PF03815; LCCL; 1.
DR SMART: SM00603; LCCL; 1.
DR PROSITE: PS50820; LCCL; 1.
KW Hypothetical protein.
SQ SEQUENCE 203 AA; 21788 MW; 363E8CF460076BBA CRC64;

Query March 24.0%; Score 163; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.8e-158;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTVLTLMKASVIEMLVLLVTGHSNKETAKKIKRPKFTVPOINCQVKAQGIIDPEFTV 60
Db 1 MRTVLTLMKASVIEMLVLLVTGHSNKETAKKIKRPKFTVPOINCQVKAQGIIDPEFTV 60
Qy 61 KCPAGCDDPKRYVGTGVYASYSVCGAAVHSGVLDNSGSKILVRYKAQSGYGSYNG 120
Db 61 KCPAGCDDPKRYVGTGVYASYSVCGAAVHSGVLDNSGSKILVRYKAQSGYGSYNG 120

OY 121 VOS1SLPRMRBSFVLESKPKKGYTPSALTYSKSPAAQAG 163
DB 121 VOS1SLPRMRBSFVLESKPKKGYTPSALTYSKSPAAQAG 163
RESULT 5
Q3T247_MOUSE PRELIMINARY; PRT; 650 AA.
ID Q3T247_MOUSE
AC Q3T247;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Adult inner ear cDNA, RIKEN full-length enriched library,
GN clone:FP930032K14 product:vtlrin, full insert sequence.
DN Name=Vtlr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Inner ear;
RA PubMed=16141073; DOI=10.1126/science.1112009;
RA Carninci P., Katayama T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Ojima R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Davis M.J., Wilmshurst L.G., Altshuler R., Allen J.E., Bailey T.L.,
RA Ambesi-Impombato A., Apweiler R., Attwood T., Ballester P., Ballester T.,
RA Banaag M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christofels A., Clutterbuck D.R.,
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RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Inner ear;
RN [3]

XX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Inner ear;
RA PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furum M., Katayama T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
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RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shimogawa A.,
RA Yeanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Inner ear;
RA PubMed=11085560; PubMed=11217851; DOI=10.1038/35055500;
RA MEDLINE=21085560; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
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RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:885-890(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Inner ear;
RA PubMed=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.


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RC STRAIN=C57BL/6J; TISSUE=inner ear;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shihara K., Itch M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itch M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=inner ear;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hoti F., Iida J., Imanura K., Imotani K., Itch M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Nishimura N.,
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RA Shihara K., Shiraki T., Tagami M., Tagami Y., Waki K., Watabiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR MGI; MGI:1921449; Vlt.
DR GO; GO:0005615; C:extracellular space; RCA.
DR InterPro; IPRO04043; LCCL.
DR InterPro; IPRO02035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PSS0820; LCCL; 1.
DR PROSITE; PSS0234; VWF_A; 2.
DR PROSITE; PSS0234; VWF_A; 2.
SQ SEQUENCE 650 AA; 70651 MW; 73D31A1B618C0719 CRC64;

Query Match 8.6%; Score 58; DB 2; Length 650;
Best Local Similarity 100.0%; Pred. No. 7.1e-50;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 78 VYASYSVCGAAVHSGVLNDSGGKILVRKVGAGSGYKGSYNGVOSLSLPRWRESF 135
Db 78 VYASYSVCGAAVHSGVLNDSGGKILVRKVGAGSGYKGSYNGVOSLSLPRWRESF 135

RESULT 6
O95LI2_BOVIN PRELIMINARY; PRT; 652 AA.
ID O95LI2_BOVIN PRELIMINARY; PRT; 652 AA.
AC O95LI2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 2.
DT 07-FEB-2006, entry version 16.
DE Vltin.
GN Name=Vltin.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_Taxid=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RA Ran Z.-X., Liu J.-G., Wayne R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; AF063832; AAL18262.2; -, mRNA.

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DR HSSP; O43405; 10BI.
DR InterPro; IPRO04043; LCCL.
DR InterPro; IPRO02035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PSS0820; LCCL; 1.
DR PROSITE; PSS0234; VWF_A; 2.
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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 77 DVYASYSVCGAAVHSGVLNDSGGKILVRKVGAGSGYKGSYNGVOSLSLPRWRESF 133
Db 77 DVYASYSVCGAAVHSGVLNDSGGKILVRKVGAGSGYKGSYNGVOSLSLPRWRESF 133

RESULT 7
O9BQ41_MOUSE PRELIMINARY; PRT; 628 AA.
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AC O9BQ41;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE 12 days embryonic spinal ganglion cDNA, RIKEN full-length enriched
DE library, clone: D130059M21 product: VITRIN homolog.
GN Name=Vltin;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX PubMed=16141072; DOI=10.1126/science.1112014;
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 RA Hayashizaki Y.,
 RT "The transcriptional landscape of the mammalian genome.",
 RL Science 309:1559-1563(2005).
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nishikido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
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 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
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 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=20493974; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
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 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer.",
 RL Genome Res. 10:1757-1771(2000).
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
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 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akiba S., Takekura Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL: AK051606; BAC34688.1; --; mRNA.
 DR HSPF, O43405; IJBI.
 DR Ensemble; ENSMUSG00000024076; Mus musculus.
 DR MGI: 1921449; Vlt.
 DR GO: GO:0005615; C:extracellular space; RCA.
 DR InterPro: IPR004043; LCCU.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam: PF03815; LCCU, 1.
 DR Pfam: PF00992; VWA, 2.
 DR PRINTS; PR00453; WVFADOMAIN.
 DR SMART; SM00603; LCCU, 1.
 DR SMART; SM00327; VWA, 2.
 DR PROSITE; PSS0820; LCCU, 1.
 DR PROSITE; PSS0234; VWF, 2.
 SQ SEQUENCE 628 AA; 68198 MW; C96C4ACEB9572480 CRC64;

Query Match 6.6%; Score 45; DB 2; Length 628;
 Best Local Similarity 100.0%; Pred. No. 1; 7e-36;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 HSGVLDNSGGKILVRKVAAGSGYKSGVNSGVQSLSPRWRESFV 135
 Db 69 HSGVLDNSGGKILVRKVAAGSGYKSGVNSGVQSLSPRWRESFV 113

RESULT 8

Q8K047_MOUSE PRELIMINARY; PRT; 650 AA.
ID Q8K047_MOUSE
AC Q8K047_MOUSE
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Vitrin.
GN Name=Vlt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rudin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Director MGC Project;
CC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL: BC034120; A034120.1; -; mRNA.
DR HSSP: O43405; IUBI.
DR Ensembl: ENSMUSG00000024076; Mus musculus.
DR MGI: MGI:1921449; Vlt.
DR GO: GO:0005615; C:extracellular space; RCA.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR02035; VWF_A.
DR Pfam: PF03815; LCCL; 1.
DR Pfam: PF00092; VMA; 2.
DR PRINTS: PR00453; VWFADOMAIN.
DR SMART: SM00603; LCCL; 1.
DR SMART: SM00327; VMA; 2.
DR PROSITE: PS50820; LCCL; 1.
DR PROSITE: PS50234; VWF_A; 2.
SQ SEQUENCE 650 AA; 70699 MW; 1641623E11003B4E CRC64;

Query Match 6.6%; Score 45; DB 2; Length 650;
Best Local Similarity 100.0%; Pred. No. 1.8e-36;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 HSGVLDSGGKILVRKVAAGSGYSGYSNGVQSLSLPRMRESFIV 135
Db 91 HSGVLDSGGKILVRKVAAGSGYSGYSNGVQSLSLPRMRESFIV 135

RESULT 9
Q8VH15_MOUSE

Q8VH15_MOUSE PRELIMINARY; PRT; 650 AA.
ID Q8VH15_MOUSE
AC Q8VH15_MOUSE
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Vitrin.
GN Name=Vlt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/C;
RA Liu J., Ren Z.-X., Takano M., Mayne R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AF454755; AAL57848.1; -; mRNA.
DR HSSP: O43405; IUBI.
DR Ensembl: ENSMUSG00000024076; Mus musculus.
DR MGI: MGI:1921449; Vlt.
DR GO: GO:0005615; C:extracellular space; RCA.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR02035; VWF_A.
DR Pfam: PF03815; LCCL; 1.
DR Pfam: PF00092; VMA; 2.
DR PRINTS: PR00453; VWFADOMAIN.
DR SMART: SM00603; LCCL; 1.
DR SMART: SM00327; VMA; 2.
DR PROSITE: PS50820; LCCL; 1.
DR PROSITE: PS50234; VWF_A; 2.
SQ SEQUENCE 650 AA; 70706 MW; FAC0F72APB953940 CRC64;

Query Match 6.6%; Score 45; DB 2; Length 650;
Best Local Similarity 100.0%; Pred. No. 1.8e-36;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 HSGVLDSGGKILVRKVAAGSGYSGYSNGVQSLSLPRMRESFIV 135
Db 91 HSGVLDSGGKILVRKVAAGSGYSGYSNGVQSLSLPRMRESFIV 135

RESULT 10
Q9CYZ1_MOUSE PRELIMINARY; PRT; 650 AA.
ID Q9CYZ1_MOUSE
AC Q9CYZ1_MOUSE
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE 10, 11 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:2810429K11 product:VITRIN, full insert sequence.
GN Name=Vlt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritsch M.C., Maeda N.,

RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chak A.M.,
 RA Chiu K.P., Choudhary V., Christofideis A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgi-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Guetlich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hall D., Hamada K., Iacono M., Ikeo K., Ikawa A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaiuchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schombach C., Sekiguchi K., Sempie C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 RA Yamamoto H., Zabarovsky E., Zhu S., Zimmer A., Zlotkin M., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki H., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.,
 RT "The transcriptional landscape of the mammalian genome.",
 RL Science 309:1559-1563(2005).
 [3]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.",
 RL Science 309:1564-1566(2005).
 [4]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC PubMed=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nakai I., Osato N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schmitt L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais K., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Savelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirose-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Aikawa T., Fukuda S.,
 RA Hara A., Haehizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [5]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC PubMed=10855660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Atakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Watanabe T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbets P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schombach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 [6]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC PubMed=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RX Shibata K., Itoh M., Aizawa K., Nagaoke S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-364-Format
 RT sequencing pipeline with 384 multicapillary sequencer",
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC PubMed=11076861; DOI=10.1101/gr.152600;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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 RT "RIKEN integrated sequence analysis (RISA) system-364-Format
 RT sequencing pipeline with 384 multicapillary sequencer",
 RL Genome Res. 10:1757-1771(2000).
 [6]
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 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC PubMed=11076861; DOI=10.1101/gr.152600;
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 RP STRAIN=C57BL/6J; TISSUE=Whole body;
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 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-364-Format
 RT sequencing pipeline with 384 multicapillary sequencer",
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC PubMed=11076861; DOI=10.1101/gr.152600;
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 RA Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
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 RT "RIKEN integrated sequence analysis (RISA) system-364-Format
 RT sequencing pipeline with 384 multicapillary sequencer",
 RL Genome Res. 10:1757-1771(2000).
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 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC PubMed=11076861; DOI=10.1101/gr.152600;
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 RT "RIKEN integrated sequence analysis (RISA) system-364-Format
 RT sequencing pipeline with 384 multicapillary sequencer",
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC PubMed=11076861; DOI=10.1101/gr.152600;
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 RP STRAIN=C57BL/6J; TISSUE=Whole body;
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 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Babbage A.;
 RL Submitted (JEB-2004) to the EMBL/GenBank/DBJ databases.
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 DR EMBL; AL596026; CAD58748.1; -; Genomic_DNA.
 DR HSSP; Q43405; 1UBI.
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 DR Pfam; PF00092; VMA; 2.
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 DT 07-FEB-2006, entry version 5.
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 RA Gardiner M.J.; Bishop R.; Shah T.; de Villiers E.P.; Carlton J.M.;
 RA Hall N.; Ren O.; Paulsen I.T.; Pain A.; Berriman M.; Wilson R.J.;
 RA Sato S.; Ralph S.A.; Mann D.J.; Xiong Z.; Shallom S.J.; Weidman J.;
 RA Jiang L.; Lynn J.; Weaver B.; Shoabli A.; Doming A.R.; Maawa D.;
 RA Crabtree J.; Wortman J.R.; Haas B.; Anguilo S.V.; Creasy T.H.; Lu C.;
 RA Suh B.; Silva J.C.; Uteback T.R.; Feldblyum T.V.; Perera M.;
 RA Allen J.; Nierman W.C.; Taracha E.L.; Salzberg S.L.; White O.R.;
 RA Fitzhugh H.A.; Morzaria S.; Venter J.C.; Fraser C.M.; Nene V.;
 RA "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
 RT Lymphocytes.";
 RL Science 309:134-137 (2005).
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 RP NUCLEOTIDE SEQUENCE.
 RA Gardiner M.; Bishop R.; Shah T.; de Villiers E.; Carlton J.M.; Hall N.;
 RA Ren O.; Paulsen I.T.; Pain A.; Berriman M.; Wilson R.J.M.; Sato S.;
 RA Ralph S.A.; Mann D.J.; Xiong Z.; Shallom S.J.; Weidman J.; Jiang L.

RA Lynn J.; Weaver B.; Shoabli A.; Maawa D.; Crabtree J.; Wortman J.R.;
 RA Haas B.; Anguilo S.; Creasy T.H.; Lu C.; Suh B.; Silva J.C.;
 RA Uteback T.; Feldblyum T.; Perera M.; Allen J.; Taracha E.L.;
 RA Salzberg S.L.; White O.; Fitzhugh H.A.; Morzaria S.; Venter J.C.;
 RA Fraser C.M.; Nene V.;
 RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 DR EMBL; AAGK01000004; EAN32150.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005044; F:scavenger receptor activity; IEA.
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 DR Pfam; PF00530; SRCR; 2.
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 RA Pain A.; Renaud H.; Berriman M.; Murphy L.; Yeats C.A.; Weir W.;
 RA Karhounou A.; Aletti M.; Bishop R.; Bouchier C.; Cochet M.;
 RA Coulson R.M.R.; Cronin A.; de Villiers E.P.; Fraser A.; Foster N.;
 RA Gardiner M.; Goble A.; Griffiths-Jones S.; Harris D.E.; Katzer F.;
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 RA Nene V.; O'Neill S.; Price C.; Quail M.A.; Rabinowitz E.;
 RA Rawlings N.D.; Rutter S.; Saunders D.; Seeger K.; Shah T.; Squares R.;
 RA Squares S.; Tivey A.; Walker A.R.; Woodward J.; Dobbelaere D.A.E.;
 RA Langsley G.; Rajandream M.-A.; McKeever D.; Shiels B.; Tait A.;
 RA Barrell B.; Hall N.;
 RT "Genome of the host-cell transforming parasite Theileria annulata
 RT compared with T. parva.";
 RL Science 309:131-133 (2005).
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DR EMBL: CR940353; CA176804.1; -: Genomic_DNA.
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 DR GO: GO:0005044; F:scavenger receptor activity; IEA.
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 DR InterPro: IPR001024; LipOase_LH2.
 DR InterPro: IPR001190; Srcr_rcpt.
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 DR pfam: PF01477; PLAT; 1.
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 DR SMART: SM00202; SR; 1.
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 DR PROSITE: PSS0095; PLAT; 1.
 DR PROSITE: PSS0287; SRCR_2; 2.
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 Db 705 HSGVLDNSGG 714

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OM protein - protein search, using sw model

Run on: June 7, 2006, 01:43:58 ; Search time 51 Seconds
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Scoring table: OLIGO
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- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6.COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7.COMB.pep.*
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- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS.COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE.COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--|
| 1 | 678 | 100.0 | 678 | 2 | US-09-991-181-179 Sequence 179, App |
| 2 | 678 | 100.0 | 678 | 2 | US-09-990-444-179 Sequence 179, App |
| 3 | 678 | 100.0 | 678 | 2 | US-09-997-333-179 Sequence 179, App |
| 4 | 678 | 100.0 | 678 | 2 | US-09-992-598-179 Sequence 179, App |
| 5 | 678 | 100.0 | 678 | 2 | US-09-988-735-179 Sequence 179, App |
| 6 | 678 | 100.0 | 678 | 3 | US-09-989-726-179 Sequence 179, App |
| 7 | 678 | 100.0 | 678 | 3 | US-09-997-514-179 Sequence 179, App |
| 8 | 678 | 100.0 | 678 | 3 | US-09-989-728-179 Sequence 179, App |
| 9 | 678 | 100.0 | 678 | 3 | US-09-997-349-179 Sequence 179, App |
| 10 | 678 | 100.0 | 678 | 3 | US-09-989-653-179 Sequence 179, App |
| 11 | 678 | 100.0 | 678 | 3 | US-09-989-293A-179 Sequence 179, App |
| 12 | 678 | 100.0 | 678 | 3 | US-09-994-264-5 Sequence 5, Appl1 |
| 13 | 678 | 100.0 | 678 | 3 | US-09-907-794A-227 Sequence 227, App |
| 14 | 678 | 100.0 | 678 | 3 | US-09-905-125A-227 Sequence 227, App |
| 15 | 678 | 100.0 | 678 | 3 | US-09-902-775A-227 Sequence 227, App |
| 16 | 678 | 100.0 | 678 | 3 | US-09-906-700-227 Sequence 227, App |
| 17 | 678 | 100.0 | 678 | 3 | US-09-579-288-2 Sequence 2, Appl1 |
| 18 | 678 | 100.0 | 678 | 3 | US-09-579-288-5 Sequence 5, Appl1 |
| 19 | 678 | 100.0 | 678 | 3 | US-09-903-603A-227 Sequence 227, App |
| 20 | 678 | 100.0 | 678 | 3 | US-09-904-920A-227 Sequence 227, App |
| 21 | 678 | 100.0 | 678 | 3 | US-09-904-016-6452 Sequence 6452, App |
| 22 | 678 | 100.0 | 678 | 3 | US-09-909-064-227 Sequence 227, App |
| 23 | 678 | 100.0 | 678 | 3 | US-09-905-381A-227 Sequence 227, App |
| 24 | 678 | 100.0 | 678 | 3 | US-09-906-618-227 Sequence 227, App |
| 25 | 678 | 100.0 | 678 | 3 | US-09-906-646-227 Sequence 227, App |
| 26 | 678 | 100.0 | 678 | 3 | US-09-904-462-227 Sequence 227, App |

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| 28 | 8 | 1.2 | 550 | 2 | US-09-906-722A-227 Sequence 227, App |
| 29 | 8 | 1.2 | 550 | 2 | US-09-905-449-227 Sequence 227, App |
| 30 | 8 | 1.2 | 550 | 2 | US-09-903-562B-227 Sequence 227, App |
| 31 | 8 | 1.2 | 550 | 2 | US-09-906-679A-227 Sequence 227, App |
| 32 | 8 | 1.2 | 550 | 3 | US-09-394-264-2 Sequence 2, Appl1 |
| 33 | 8 | 1.2 | 550 | 3 | US-09-907-841-227 Sequence 227, App |
| 34 | 8 | 1.2 | 552 | 3 | US-09-394-264-7 Sequence 8845, App |
| 35 | 8 | 1.2 | 568 | 2 | US-09-949-016-8845 Sequence 8845, App |
| 36 | 8 | 1.2 | 575 | 2 | US-09-949-016-8294 Sequence 8294, App |
| 37 | 8 | 1.2 | 733 | 2 | US-09-270-767-41626 Sequence 41626, App |
| 38 | 8 | 1.0 | 27 | 3 | US-09-463-058-178 Sequence 178, App |
| 39 | 7 | 1.0 | 62 | 2 | US-09-621-976-6538 Sequence 6538, App |
| 40 | 7 | 1.0 | 27 | 3 | US-09-248-796A-23281 Sequence 23281, App |
| 41 | 7 | 1.0 | 65 | 2 | US-09-513-999C-7765 Sequence 7765, App |
| 42 | 7 | 1.0 | 71 | 2 | US-09-248-796A-23031 Sequence 23031, App |
| 43 | 7 | 1.0 | 73 | 2 | US-09-488-039A-13279 Sequence 13279, App |
| 44 | 7 | 1.0 | 92 | 2 | US-09-270-767-59560 Sequence 59560, App |
| 45 | 7 | 1.0 | 99 | 2 | US-09-270-767-60317 Sequence 60317, App |

ALIGNMENTS

RESULT 1
US-09-991-181-179
Sequence 179, Application US/09991181
Patent No. 6913919
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Deonoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/045787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 2; Length 678;
Best Local Similarity 100.0%; Pct Ident 100.0%; Mismatches 0; Indels 0; Gaps 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 VQSLSPRMRESFVLESKPKGVTPSALTYSKSPAAQAGETTKAYQRPPIGTAAQ 180
DB 121 VQSLSPRMRESFVLESKPKGVTPSALTYSKSPAAQAGETTKAYQRPPIGTAAQ 180
QY 181 PVTLMQLAATVAVATPTTLPRPSPASATTSIPRPOSVGHRSGEMDLMTATYTSSQNR 240
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DB 241 PRADPGIQRDPSCGAARQKVGADVSLGLVPEKELSTQSLPVSIGDPNCKIDSLFIDG 300
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RESULT 2
US-09-990-444-179
Sequence 179, Application US/09990444
Patent No. 6930170
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleon
APPLICANT: Fong, Sherman

;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C19
;; CURRENT APPLICATION NUMBER: US/09/990,444
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MRTVVLTMKASVIEMLVLLVLTGSHSNKETAKKIKRPFVTPQINCVDVAKIIDEFFIV 60
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Db
QY 121 VQSLSPRMRESFIVIESKPKKGVTPSALTYSKSPAAQGETTKAYORPPIPGTTAQ 180
121 VQSLSPRMRESFIVIESKPKKGVTPSALTYSKSPAAQGETTKAYORPPIPGTTAQ 180
Db
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121 VQSLSPRMRESFIVIESKPKKGVTPSALTYSKSPAAQGETTKAYORPPIPGTTAQ 180
Db
QY 181 PVTIMOLLAVTAVATPTTLPRPSPAASTTSIPRQSVGHSQENDLWSTATYSSQNR 240
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Db
QY 241 PRADPGIQRQDPGGAFAQKRVGADVSLGLVPKEELSTQSLSEPVSLDDPNCKIDLSPIDG 300
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Db

Fri Jun 9 11:08:02 2006

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Db 421 GINIFPTIEGAENKEKYVVEPNPANKAVCTGCFYSLHQSWGLKHTLOPLVKRCD 480
QY 481 TDRLACSKTCNSADIGVIDGSSVGTGNFRVYQFVTNLTKREISDTPRIGAVOYT 540
Db 481 TDRLACSKTCNSADIGVIDGSSVGTGNFRVYQFVTNLTKREISDTPRIGAVOYT 540
QY 541 YEORLEFGFDKYSKPDILNAIKRVYWSGGTSTGAINFALFQLEFKSKENKRLMLI 600
Db 541 YEORLEFGFDKYSKPDILNAIKRVYWSGGTSTGAINFALFQLEFKSKENKRLMLI 600
QY 601 TDGSRYSYDVRIPAMAHLKGVITTAIGVMAAOEELVIAITHPADHSFPVDEPNLHOY 660
Db 601 TDGSRYSYDVRIPAMAHLKGVITTAIGVMAAOEELVIAITHPADHSFPVDEPNLHOY 660
QY 661 VPRIIIONCTEFNSOPRN 678
Db 661 VPRIIIONCTEFNSOPRN 678

RESULT 3
US-09-997-333-179
Sequence 179, Application US/09997333
Patent No. 6953836
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Bacon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C27
CURRENT APPLICATION NUMBER: US/09/997,333
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR APPLICATION NUMBER: 60/0091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/0091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/0091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/0092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRTVLTMTKASVIEMLVLLVTGVSHKETAKKIKRPFVPOINCDVKAKGIIDPEFIY 60
Qy 61 KCPAGCDDPKYHYGVGVVSVSSVCGAASHSVLNSGGKILVRKVAQSGYKGSYNG 120
Db 61 KCPAGCDDPKYHYGVGVVSVSSVCGAASHSVLNSGGKILVRKVAQSGYKGSYNG 120
Qy 121 VQSLSPRMRSEFTVLESKPKKGVTPSALTYSKSPAQAQETTKAYORPPIPGTTAQ 180
Db 121 VQSLSPRMRSEFTVLESKPKKGVTPSALTYSKSPAQAQETTKAYORPPIPGTTAQ 180
Qy 181 PVTLMQLAVTVAVATPTTLPRPSPAASSTSIIPROSVGHSQEMDLWSTATYTSQNR 240
Db 181 PVTLMQLAVTVAVATPTTLPRPSPAASSTSIIPROSVGHSQEMDLWSTATYTSQNR 240
Qy 241 PRADPGIQRODPSGAAPQKVGADVSLGLVPKELSQSLSEPLSDPNCKIDLSFLIDG 300
Db 241 PRADPGIQRODPSGAAPQKVGADVSLGLVPKELSQSLSEPLSDPNCKIDLSFLIDG 300
Qy 301 STSISGRFRPIQKQLADVAQALDIGPAGPLMGVVOYGDNPATHFNLKHTNSRDLKTAI 360
Db 301 STSISGRFRPIQKQLADVAQALDIGPAGPLMGVVOYGDNPATHFNLKHTNSRDLKTAI 360
Qy 361 EKITRGGLSNVGRASIFVTXNFFSKANGRSAPNVVVVMDGPTDKYKESRLARES 420
Db 361 EKITRGGLSNVGRASIFVTXNFFSKANGRSAPNVVVVMDGPTDKYKESRLARES 420
Qy 421 GINIFFTIEGAENENQYVEEPPNKAACRNGEFLSHVQSGFGLKTLQPLVXKVC 480
Db 421 GINIFFTIEGAENENQYVEEPPNKAACRNGEFLSHVQSGFGLKTLQPLVXKVC 480
Qy 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFTVNLTKPEFISDTRIGAVOYT 540
Db 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFTVNLTKPEFISDTRIGAVOYT 540
Qy 541 YEORLEFGFDKYSKPDILNAIKRVGVWSGSTGAALNFALQLEFKSKPNRKMLILI 600
Db 541 YEORLEFGFDKYSKPDILNAIKRVGVWSGSTGAALNFALQLEFKSKPNRKMLILI 600
Qy 601 TDRGSYDVARIPMAAHLKGVITTYATGVMAAEELEVIATHPARHSPFVDEFDNLHOY 660
Db 601 TDRGSYDVARIPMAAHLKGVITTYATGVMAAEELEVIATHPARHSPFVDEFDNLHOY 660
Qy 661 VPRIIQNICTEFNSOPRN 678
Db 661 VPRIIQNICTEFNSOPRN 678

RESULT 4
US-09-992-598-179
; Sequence 179, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C20
CURRENT FILING DATE: US/09/1992, 598
PRIOR APPLICATION NUMBER: 2001-11-14
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 0; Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 KCPAGCDDPKHYHYGTIVYASYSVCGAAVHSGVLNDSGGKILYRKVAGSGYGSYSNG 120
QY 121 VQSLSPRMRESFVLESKRKGGVTPSALTYSSSKSPAAOAGETTAAYORPPITGTTAQ 180
DB 121 VQSLSPRMRESFVLESKRKGGVTPSALTYSSSKSPAAOAGETTAAYORPPITGTTAQ 180
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DB 181 PVTLMQALATVAVATPTTLPRPSPASATTSIPRPOSVGHRSGEMDLMTATYTSSQNR 240
QY 241 PRADPGIQRDPGSAAGQKVGADVSLGLVPKEKLSFQSLSEPVSLGDPNCKIDISFLIDG 300
DB 241 PRADPGIQRDPGSAAGQKVGADVSLGLVPKEKLSFQSLSEPVSLGDPNCKIDISFLIDG 300
QY 301 STSIGKRFRPIQKQLADVAQALDIGPAGPLMGVVQYGDNPATHTFNLTHTNSKDLTAT 360
DB 301 STSIGKRFRPIQKQLADVAQALDIGPAGPLMGVVQYGDNPATHTFNLTHTNSKDLTAT 360

QY 361 EKITQRGGLSNVGRALISFVTKNFFSSKANGRSGAPNVVVVMDGMPDTDKVEASRLARES 420
DB 361 EKITQRGGLSNVGRALISFVTKNFFSSKANGRSGAPNVVVVMDGMPDTDKVEASRLARES 420
QY 421 GINFFITTEGAAENENQYVVEPFAKAVCRNNGPFSLSHVQSMFGJHKTLOPLVXRVC 480
DB 421 GINFFITTEGAAENENQYVVEPFAKAVCRNNGPFSLSHVQSMFGJHKTLOPLVXRVC 480
QY 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFTVNLTKFEFISDTRIGAVQYT 540
DB 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFTVNLTKFEFISDTRIGAVQYT 540
QY 541 YEOBLEFDPKYSKPDILNAIKRVGYSGGTSGAINFALBQLEFKSKIPNKRKLMILI 600
DB 541 YEOBLEFDPKYSKPDILNAIKRVGYSGGTSGAINFALBQLEFKSKIPNKRKLMILI 600
QY 601 TDGRSYDDVRIIPMAAHLKGVITTAIGVAAQOELEVIATHPARHSPFVDEFDNLHOY 660
DB 601 TDGRSYDDVRIIPMAAHLKGVITTAIGVAAQOELEVIATHPARHSPFVDEFDNLHOY 660
QY 661 VPRIONICTEFSNOPEN 678
DB 661 VPRIONICTEFSNOPEN 678

RESULT 5

US-09-989-735-179

Sequence 179, Application US/09989735

Patent No. 6972185

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gottlisen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC61

CURRENT APPLICATION NUMBER: US/09/989, 735

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

[illegible]

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTLMKASVEMFLVLTGVSNNKETAKTKRPFYTPQINCDVKAGKIIDPEFIV 60
DB 1 MRTVLTLMKASVEMFLVLTGVSNNKETAKTKRPFYTPQINCDVKAGKIIDPEFIV 60
QY 61 KCPAGCDDPKHYVGTDVASYSVSCGAHVHSGVLNDSSGKILVRKVAQSGYKGSYNG 120
DB 61 KCPAGCDDPKHYVGTDVASYSVSCGAHVHSGVLNDSSGKILVRKVAQSGYKGSYNG 120
QY 121 VQSLSLPRMBSPFLVLESKPKKGYTPSALTYSSSKSPAQAQETTKAYQRPPIPGTTAQ 180
DB 121 VQSLSLPRMBSPFLVLESKPKKGYTPSALTYSSSKSPAQAQETTKAYQRPPIPGTTAQ 180
QY 181 PVTLMQLAATVAAVPTTLPRSPSAASTTISIRPOSVGHRSQEMDLMSTATYSSQNR 240
DB 181 PVTLMQLAATVAAVPTTLPRSPSAASTTISIRPOSVGHRSQEMDLMSTATYSSQNR 240
QY 241 PRADPGIORDPSGAFAQKPVGADVSLGLVPKEELSTQSLSPVSLGDPNCKIDSLFLDG 300
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DB 301 STSISGKRFRIOKQLLDVAQALDIGRAGPLMGVVOYQDNPAITHFNKTHNSDLKTAI 360
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DB 421 GINIFITIEGAANEKQYVVEPNFANKAVCRITNGFYSLHVSQWFGHLKTLQPLVKVCD 480
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QY 601 TDRGRSYDVARI PAMAAHLKGVITTAIGVAAAQEELEVIATHPARDHSFVDEFDNLHOY 660
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DB 661 VPRIIIONICTEFSQPRN 678

RESULT 6
US-09-989-726-179
Sequence 179, Application US/09989726
Patent No. 701811

;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Demoyers, Luc
;; APPLICANT: Eaton, Dan L.

;; APPLICANT: Ferrara, Napoleone
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;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
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;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C60
;; CURRENT APPLICATION NUMBER: US/09/989,726
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRYVVLTMKASVLEMFVLVLVTGHSNKEKTAKKIKRKFTVPQINCVCVKGKIIDPERIV 60
Qy 61 KCPAGCDDPKYHYGTGVVAVSYSSVCGAAVHSGVLDSGGKILVRKAVAGSGYGSYNG 120
Db 61 KCPAGCDDPKYHYGTGVVAVSYSSVCGAAVHSGVLDSGGKILVRKAVAGSGYGSYNG 120
Qy 121 VQSLPRMRRESFVLESKPKKGVTPSALTYSSSKSPAAOAGETTKAYORPPIGTAAQ 180
Db 121 VQSLPRMRRESFVLESKPKKGVTPSALTYSSSKSPAAOAGETTKAYORPPIGTAAQ 180
Qy 181 PVTLMQLLATVVAATPTLPRPSPASSTTSIPRPSVGHRSQEMLMSTATYTSSONR 240
Db 181 PVTLMQLLATVVAATPTLPRPSPASSTTSIPRPSVGHRSQEMLMSTATYTSSONR 240
Qy 241 PRADPGIQODPSSGAQKXVGVADVSLGLVPKEELSTQSLSPVSLGDPNCKIDLSFLIDG 300
Db 241 PRADPGIQODPSSGAQKXVGVADVSLGLVPKEELSTQSLSPVSLGDPNCKIDLSFLIDG 300
Qy 301 STSIGKRFRIOKQLADVAQALDIGPAGPLMGVQYGDNPATHFNLKHTNSDLXTAI 360
Db 301 STSIGKRFRIOKQLADVAQALDIGPAGPLMGVQYGDNPATHFNLKHTNSDLXTAI 360

Db 301 STSIGRRFRIOQLADVAQALDIGPAGPLMGVVOYGDNPATHPNLKTHNSDLKTAI 360
QY 361 EKITORGGLSNVGRALISFTVKNFPSKANGNSGAPNVVVVVVDGMPDTKYEAARLARES 420
Db 361 EKITORGGLSNVGRALISFTVKNFPSKANGNSGAPNVVVVVVDGMPDTKYEAARLARES 420
QY 421 GINIFITIEGAANEKQYVVEPNFANKAVCRITNGFYSLSHVQSWFGLHKTLOPLVKRVC 480
Db 421 GINIFITIEGAANEKQYVVEPNFANKAVCRITNGFYSLSHVQSWFGLHKTLOPLVKRVC 480
QY 481 TDLRACSKTLLNSADIGFVIDGSSVGTGNFRITLQVTVNLTKFEFISDTRIGAVOYT 540
Db 481 TDLRACSKTLLNSADIGFVIDGSSVGTGNFRITLQVTVNLTKFEFISDTRIGAVOYT 540
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Db 541 YEORLEGFPGKYSKSPILNAIKRVGWSGSGTSGAALNFBOLFKSKPKNKKMLILI 600
QY 601 TDRSVDVRIIPMAAHLKGVITVAIGVAMAAQEELEVIATHPARDHSFVDEFDNLHOY 660
Db 601 TDRSVDVRIIPMAAHLKGVITVAIGVAMAAQEELEVIATHPARDHSFVDEFDNLHOY 660
QY 661 VPRIIQNICTEFNSQPRN 678
Db 661 VPRIIQNICTEFNSQPRN 678

RESULT 7

US-09-997-514-179
Sequence 179, Application US/09997514
Patent No. 7019116
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C46
CURRENT APPLICATION NUMBER: US/09/997,514
CURRENT FILING DATE: 2001-11-15
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PRIOR FILING DATE: 1998-07-09

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QY 301 STSICGRFRIOKLLADVAQALDIGAGPLMGVVOYGDNPATFNLKTHNSRDLKTAI 360
DB 301 STSICGRFRIOKLLADVAQALDIGAGPLMGVVOYGDNPATFNLKTHNSRDLKTAI 360
QY 361 EKITORGSLNVGSAISFVTNKFPSKANGNSGAPNVVWVDMPTDKVEASRLARES 420
DB 361 EKITORGSLNVGSAISFVTNKFPSKANGNSGAPNVVWVDMPTDKVEASRLARES 420
QY 421 GINIFFTIEGAANENQYVVEPNFANKAVCRITNGFYSLHVQSWFGLHKTLOPLVKRCD 480
DB 421 GINIFFTIEGAANENQYVVEPNFANKAVCRITNGFYSLHVQSWFGLHKTLOPLVKRCD 480
QY 481 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRYVLOFVTNLTKEFEISDTRIGAVOYT 540
DB 481 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRYVLOFVTNLTKEFEISDTRIGAVOYT 540
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DB 541 YEOLEFGFPDKYSKPIILNAIKRVGWSGTSGAALNFALEDFPKSKPKXKMLMI 600
QY 601 TDGSSYDDVRIPAAALHKVITYTAIGVMAAQEELVIATHPARDHSFFVDEFDNLHQY 660
DB 601 TDGSSYDDVRIPAAALHKVITYTAIGVMAAQEELVIATHPARDHSFFVDEFDNLHQY 660
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DB 661 VPRILIONICTEFSQPNR 678

RESULT 8
US-09-989-728-179
Sequence 179, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730F1C72
CURRENT APPLICATION NUMBER: US/09/989,728
CURRENT FILING DATE: 2001-11-20
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLVTLMKASVIEMLVLLVTVGHSNKEITAKKIKRPFVTPQINCVDKAKIIDPEFIY 60
DB 1 MRTLVTLMKASVIEMLVLLVTVGHSNKEITAKKIKRPFVTPQINCVDKAKIIDPEFIY 60
QY 61 KCPAGCDDPKHYHGVGDVVASYSVCGAAVHSGVLNDSGGKILVRYKAAQSGVGSYNSG 120
DB 61 KCPAGCDDPKHYHGVGDVVASYSVCGAAVHSGVLNDSGGKILVRYKAAQSGVGSYNSG 120
QY 121 VQSLSLPRWRESFVLESKPKKGVTPSALTYSKSPAAQAGETTRAYORPPIPGTTAAQ 180
DB 121 VQSLSLPRWRESFVLESKPKKGVTPSALTYSKSPAAQAGETTRAYORPPIPGTTAAQ 180
QY 181 PVLIMQLAAVTVAATPTTLPRPSPASATTSIPRPOSVGHRSQEMDLWSTATYTSSQNR 240
DB 181 PVLIMQLAAVTVAATPTTLPRPSPASATTSIPRPOSVGHRSQEMDLWSTATYTSSQNR 240
QY 241 PRADPGIQRDDPSGAARQKPYGAVSLGLVPKKELTQSLSEPVSLGDPNCKIDISFLIDG 300
DB 241 PRADPGIQRDDPSGAARQKPYGAVSLGLVPKKELTQSLSEPVSLGDPNCKIDISFLIDG 300
QY 301 STSIGKRFRRIQKQLADVAQALDIGPAGPLMGVGVYGDNPATHFNLKTHNSRDLXTAI 360

DB 301 STSIGKRFRRIQKQLADVAQALDIGPAGPLMGVGVYGDNPATHFNLKTHNSRDLXTAI 360
QY 361 EKITQRGGLSNVGALISFVTKNFKFSKANGRSRGA PNVMVWVDMQPDVKEEARLRES 420
DB 361 EKITQRGGLSNVGALISFVTKNFKFSKANGRSRGA PNVMVWVDMQPDVKEEARLRES 420
QY 421 GINIFFTITGGAENEQYVVEPNFANKAVCRTGFSLSHVQSWFGJLHKTLOPLVKEVCD 480
DB 421 GINIFFTITGGAENEQYVVEPNFANKAVCRTGFSLSHVQSWFGJLHKTLOPLVKEVCD 480
QY 481 TDLRACSKTCLNSADIGFVIDSSSVGTGNFRVLOFTVNLTKFEISDTDRIGAVOYT 540
DB 481 TDLRACSKTCLNSADIGFVIDSSSVGTGNFRVLOFTVNLTKFEISDTDRIGAVOYT 540
QY 541 YEORLFEGFDKYSKPKPILNAIKRVGVWSGSTGGA INFALQLEFKSKRPNKRKMLI 600
DB 541 YEORLFEGFDKYSKPKPILNAIKRVGVWSGSTGGA INFALQLEFKSKRPNKRKMLI 600
QY 601 TDRGSYDVRILPMAAHLKGVITYAIGVAAQEELEVIATHPARDHSFVDEFDNLHOY 660
DB 601 TDRGSYDVRILPMAAHLKGVITYAIGVAAQEELEVIATHPARDHSFVDEFDNLHOY 660
QY 661 VPRILIONICTEPNSQPRN 678
DB 661 VPRILIONICTEPNSQPRN 678

RESULT 9
US-09-997-349-179
; Sequence 179, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC37
; CURRENT APPLICATION NUMBER: US/09/997,349
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945

[illegible]

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTMKASVIEMLVLTGHSNKETAKKIKRPFYTPQINCVDYKAGKIIDPEFIV 60
DB 1 MRTVLTMKASVIEMLVLTGHSNKETAKKIKRPFYTPQINCVDYKAGKIIDPEFIV 60

QY 61 KCPAGCDDPKYHVGTGVYASVSSVCGAAVHSGVLNDGSGKILVRKVAAGSGYGSVNG 120
DB 61 KCPAGCDDPKYHVGTGVYASVSSVCGAAVHSGVLNDGSGKILVRKVAAGSGYGSVNG 120

QY 121 VQSLPRMRESFVLESKPKKGYTPSALTYSKSPAAQAGETTKAYQRPPIGTTAQ 180
DB 121 VQSLPRMRESFVLESKPKKGYTPSALTYSKSPAAQAGETTKAYQRPPIGTTAQ 180

QY 181 PVTIMOLLAVTVAATPTLPRSPSAASTTSIPRPOSVGHRSQEMDIWSTATTYSSQNR 240
DB 181 PVTIMOLLAVTVAATPTLPRSPSAASTTSIPRPOSVGHRSQEMDIWSTATTYSSQNR 240

QY 241 PRADPGIORODPSGAFOKPYGADVSLGLVPEKEELSTQSLSPVSLGDNCKIDISPLIDG 300
DB 241 PRADPGIORODPSGAFOKPYGADVSLGLVPEKEELSTQSLSPVSLGDNCKIDISPLIDG 300

QY 301 STSICKRRFRIOKQLADVAQALDIGPAGPLMGVVOYGDNPATHTFNLKTHNSRDLKTAI 360
DB 301 STSICKRRFRIOKQLADVAQALDIGPAGPLMGVVOYGDNPATHTFNLKTHNSRDLKTAI 360

QY 361 EKITQRGGLSNVGAISFVTKNFPSKANGNSGAPNVVVVWDGMPIDKVEASRLAES 420
DB 361 EKITQRGGLSNVGAISFVTKNFPSKANGNSGAPNVVVVWDGMPIDKVEASRLAES 420

QY 421 GINIFFTTIGGAENEMQYVVEPNPANKAVCRITGFVSLHVSQWFGHLKTLQPLVKRYCD 480
DB 421 GINIFFTTIGGAENEMQYVVEPNPANKAVCRITGFVSLHVSQWFGHLKTLQPLVKRYCD 480

QY 481 TDRACSKTCUNSDADIGFVIDGSSSVGTGNFRVLQFVTNLTKFEELSDTDRIGAVQYT 540
DB 481 TDRACSKTCUNSDADIGFVIDGSSSVGTGNFRVLQFVTNLTKFEELSDTDRIGAVQYT 540

QY 541 YEQRLERGFDPKYSKPDILNAIKRKGVSQGTSTGAALNFALBOLFKXSKPKKKMLILI 600
DB 541 YEQRLERGFDPKYSKPDILNAIKRKGVSQGTSTGAALNFALBOLFKXSKPKKKMLILI 600

QY 601 TDGSSYDVRIPMAAHLKGVITAIAGVMAAOELEVIAHPARDHSFFVDEEDNLHQY 660
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QY 661 VPRIIQICTEFNSQPRN 678
DB 661 VPRIIQICTEFNSQPRN 678

RESULT 10
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; Sequence 179, Application US/09997653
; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David

;; APPLICANT: Deenoyers, Luc
;; APPLICANT: Eacron, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerlitsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
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;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Collin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 3; Length 678;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVVLTMKASVTEMFLVLLVTVGSHNKETAKKIKPKKTVPPQINDVAKGIIDPEFV 60
DB 1 MTRVVLTMKASVTEMFLVLLVTVGSHNKETAKKIKPKKTVPPQINDVAKGIIDPEFV 60
QY 1 KCPAGCOPDKYHYGTDVYASYSVCCAAVHSGVLNDSGKILVRKAGOSGYKSYSNG 120
DB 1 KCPAGCOPDKYHYGTDVYASYSVCCAAVHSGVLNDSGKILVRKAGOSGYKSYSNG 120
QY 121 VQSLSPRMRESFIVLESKPKKGVTPSALTYSSSKSPAAGETTKAYORPPIPGTTAQ 180
DB 121 VQSLSPRMRESFIVLESKPKKGVTPSALTYSSSKSPAAGETTKAYORPPIPGTTAQ 180
QY 181 PVTLMQLLAVTVAVAPPTLPRSPSAASTTSIPROQSVGHRQEMDLWSTATYSSQNR 240
DB 181 PVTLMQLLAVTVAVAPPTLPRSPSAASTTSIPROQSVGHRQEMDLWSTATYSSQNR 240
QY 241 PRADPGIORODPSGAFFORPVGADVSLGLVPKEELSTOSLEPVSLGDPNCKIDLSEFLIDG 300
DB 241 PRADPGIORODPSGAFFORPVGADVSLGLVPKEELSTOSLEPVSLGDPNCKIDLSEFLIDG 300

QY 301 STIGKRRFRIOKOLLADVAQALDIPGAPLMGVQGDNPATHTNLTHTNSRDLKTAI 360
D 301 STIGKRRFRIOKOLLADVAQALDIPGAPLMGVQGDNPATHTNLTHTNSRDLKTAI 360
QY 361 EKITORGLSNVGAISFVTNKFPSKANGNSGAPNVVVVVWDGMPDQKVEASRLAES 420
D 361 EKITORGLSNVGAISFVTNKFPSKANGNSGAPNVVVVVWDGMPDQKVEASRLAES 420
QY 421 GINFFTTIEGAANENQYVVEPNPANKAVRTGTFPSLHVQSWFGHLKTLQPLVKVCD 480
D 421 GINFFTTIEGAANENQYVVEPNPANKAVRTGTFPSLHVQSWFGHLKTLQPLVKVCD 480
QY 481 TDRACKCTCLNSADIGFVIDGSSVGTGNFRVLQFVTNLTKFEISDTRIGAVOYT 540
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QY 541 YEORLFEGFDKYSKSPDLNNAIKKVGWYSGSTGGAINFALQPLFKSKPKNKKMLILI 600
D 541 YEORLFEGFDKYSKSPDLNNAIKKVGWYSGSTGGAINFALQPLFKSKPKNKKMLILI 600
QY 601 TDGSRVYDVRIPMAAHLKGVITTAIGVMAAOELEVIAITHPARDSFFVDEPDNLHOY 660
D 601 TDGSRVYDVRIPMAAHLKGVITTAIGVMAAOELEVIAITHPARDSFFVDEPDNLHOY 660
QY 661 VPRIONICTEFPNSOPRN 678
D 661 VPRIONICTEFPNSOPRN 678

RESULT 11
US-09-989-293A-179
Sequence 179, Application US/09989293A
Patent No. 7034136
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: KJlavin, Ivar J.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989, 293A
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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DB 121 VQSLSPRMRESFVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
QY 181 PVTLMQILANTVAVAPPTLPSPSPAASSTSIIPROSVCHROEMDINSTATYSSONR 240
DB 181 PVTLMQILANTVAVAPPTLPSPSPAASSTSIIPROSVCHROEMDINSTATYSSONR 240
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DB 241 PRADPGIORODPSGAFAFOKVGADVSLGLVPKEELSTOSLEPVSIGDPNCKIDLSFLIDG 300
QY 301 STSIGRRFRIOKQILADVAAQALDIGPAGPLMGVVOYGDNPAHFNLKHTNSRDLKTAI 360
DB 301 STSIGRRFRIOKQILADVAAQALDIGPAGPLMGVVOYGDNPAHFNLKHTNSRDLKTAI 360
QY 361 EKITRGGSINVRRAISFVTKNFFSKANGRSRAPVVVVVVVGVGWPDKVEASRLARES 420
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DB 601 TDRGSYDDVRIIPMAAHLKGVITYAIGVAMAAQEBLEVIATHPARDSPFVDFDNLHOY 660
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; Sequence 5, Application US/09394264
; Patent No. 7030235
; GENERAL INFORMATION:
; APPLICANT: Morton, Cynthia C.
; APPLICANT: Robertson, Nahid G.

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; TITLE OF INVENTION: NOVEL COCHLEAR GENE COCH5B2 AND USES THEREOF
; FILE REFERENCE: 10286/008001
; CURRENT APPLICATION NUMBER: US/09/394,264
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: US 60/102,343
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
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US-09-394-264-5

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Best Local Similarity 100.0%; Pred. No. 18;
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Db      7  IDGSSSVG 14

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; Sequence 227, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20344
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; NUMBER OF SEQ ID NOS: 423
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; ORGANISM: Homo sapiens
US-09-907-794A-227

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RESULT 14
US-09-905-125A-227
; Sequence 227, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
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; NUMBER OF SEQ ID NOS: 423
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US-09-905-125A-227
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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavrin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-10
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; ORGANISM: Homo sapiens
US-09-902-775A-227
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GenCore version 5.1.9
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OM protein - protein search, using sw model

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 562 | 678 | 100.0 | 678 | 4 | US-10-174-587-150 Sequence 150, App |
| 626 | 678 | 100.0 | 678 | 4 | US-10-063-742-34 Sequence 34, App1 |
| 741 | 678 | 100.0 | 678 | 5 | US-10-972-317-34 Sequence 34, App1 |
| 743 | 678 | 100.0 | 678 | 5 | US-10-950-374-179 Sequence 179, App |
| 751 | 678 | 100.0 | 678 | 6 | US-11-102-240-34 Sequence 34, App1 |
| 752 | 678 | 100.0 | 678 | 6 | US-11-103-195-34 Sequence 34, App1 |
| 753 | 411 | 60.6 | 693 | 4 | US-10-408-765A-2507 Sequence 2507, App |
| 754 | 328 | 48.4 | 329 | 3 | US-09-732-227-2 Sequence 2, App1 |
| 755 | 328 | 48.4 | 329 | 4 | US-10-127-101-2 Sequence 2, App1 |
| 756 | 259 | 38.2 | 656 | 3 | US-09-801-736A-2 Sequence 2, App1 |
| 757 | 178 | 26.3 | 178 | 3 | US-09-801-736A-4 Sequence 4, App1 |
| 758 | 172 | 25.4 | 172 | 3 | US-09-864-761-47637 Sequence 47637, App |
| 759 | 171 | 25.2 | 171 | 3 | US-09-864-761-33310 Sequence 33310, App |
| 760 | 161 | 23.7 | 186 | 3 | US-09-764-870-301 Sequence 301, App |
| 761 | 161 | 23.7 | 186 | 3 | US-09-764-875-797 Sequence 797, App |
| 762 | 161 | 23.7 | 186 | 4 | US-10-125-540-501 Sequence 301, App |
| 763 | 84 | 12.4 | 160 | 4 | US-09-801-736A-3 Sequence 3, App1 |
| 764 | 75 | 11.1 | 75 | 3 | US-09-864-761-33306 Sequence 33306, App |
| 765 | 75 | 11.1 | 75 | 3 | US-09-864-761-38418 Sequence 38418, App |
| 766 | 63 | 9.3 | 64 | 3 | US-09-864-761-48690 Sequence 48690, App |
| 767 | 63 | 9.3 | 64 | 3 | US-09-864-761-49053 Sequence 49053, App |
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| 769 | 9 | 1.3 | 224 | 5 | US-10-450-763-46497 Sequence 46497, App |
| 770 | 8 | 1.2 | 72 | 4 | US-10-437-963-164114 Sequence 164114, App |
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| 1468 | 7 | 1.0 | 113 | 5 | US-10-729-441-85 | Sequence 85, Appl |
| 1469 | 7 | 1.0 | 113 | 5 | US-10-729-441-86 | Sequence 86, Appl |
| 1470 | 7 | 1.0 | 113 | 5 | US-10-729-441-80 | Sequence 90, Appl |
| 1471 | 7 | 1.0 | 113 | 5 | US-10-729-441-94 | Sequence 94, Appl |
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| 1474 | 7 | 1.0 | 113 | 5 | US-10-897-406-11 | Sequence 11, Appl |
| 1475 | 7 | 1.0 | 113 | 5 | US-10-897-406-12 | Sequence 12, Appl |
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| 1497 | 7 | 1.0 | 128 | 6 | US-11-096-568A-1053 | Sequence 1053, Ap |
| 1498 | 7 | 1.0 | 129 | 4 | US-10-425-114-69213 | Sequence 69213, A |
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Job time : 208 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 7, 2006, 01:56:23 ; Search time 16 Seconds
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Title: US-10-063-540-34

Perfect score: 678

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 58871 seqs, 1156156 residues

Word size : 6

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1 | 678 | 100.0 | 678 | US-10-196-749-150 | Sequence 150, App |
| 2 | 678 | 100.0 | 678 | US-11-101-316-34 | Sequence 34, App |
| 3 | 8 | 1.2 | 503 | US-11-293-697-4497 | Sequence 4497, App |
| 4 | 8 | 1.2 | 550 | US-10-196-749-46 | Sequence 46, App |
| 5 | 7 | 1.0 | 91 | US-10-953-349-36732 | Sequence 36732, A |
| 6 | 7 | 1.0 | 99 | US-10-953-349-37027 | Sequence 37027, A |
| 7 | 7 | 1.0 | 126 | US-10-953-349-30530 | Sequence 30530, A |
| 8 | 7 | 1.0 | 128 | US-10-953-349-37026 | Sequence 37026, A |
| 9 | 7 | 1.0 | 142 | US-10-953-349-37025 | Sequence 37025, A |
| 10 | 7 | 1.0 | 170 | US-10-953-349-30529 | Sequence 30529, A |
| 11 | 7 | 1.0 | 185 | US-10-953-349-28247 | Sequence 28247, A |
| 12 | 7 | 1.0 | 202 | US-10-953-349-30528 | Sequence 30528, A |
| 13 | 7 | 1.0 | 217 | US-10-953-349-31820 | Sequence 31820, A |
| 14 | 7 | 1.0 | 246 | US-10-953-349-18707 | Sequence 18707, A |
| 15 | 7 | 1.0 | 247 | US-10-953-349-31819 | Sequence 31819, A |
| 16 | 7 | 1.0 | 255 | US-10-953-349-20680 | Sequence 20680, A |
| 17 | 7 | 1.0 | 263 | US-10-953-349-20679 | Sequence 20679, A |
| 18 | 7 | 1.0 | 264 | US-10-953-349-20678 | Sequence 20678, A |
| 19 | 7 | 1.0 | 265 | US-10-953-349-28246 | Sequence 28246, A |
| 20 | 7 | 1.0 | 277 | US-10-953-349-18706 | Sequence 18706, A |
| 21 | 7 | 1.0 | 281 | US-10-953-349-18705 | Sequence 18705, A |
| 22 | 7 | 1.0 | 295 | US-10-953-349-23677 | Sequence 23677, A |
| 23 | 7 | 1.0 | 310 | US-11-305-413-9 | Sequence 9, Appl |
| 24 | 7 | 1.0 | 334 | US-10-953-349-28245 | Sequence 28245, A |
| 25 | 7 | 1.0 | 352 | US-10-953-349-37513 | Sequence 37513, A |

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| 26 | 7 | 1.0 | 353 | US-10-953-349-32102 | Sequence 32102, A |
| 27 | 7 | 1.0 | 391 | US-10-953-349-8752 | Sequence 8752, Ap |
| 28 | 7 | 1.0 | 413 | US-10-953-349-7231 | Sequence 7231, Ap |
| 29 | 7 | 1.0 | 413 | US-10-953-349-11011 | Sequence 11011, A |
| 30 | 7 | 1.0 | 444 | US-10-953-349-37512 | Sequence 37512, A |
| 31 | 7 | 1.0 | 446 | US-10-953-349-32101 | Sequence 32101, A |
| 32 | 7 | 1.0 | 447 | US-10-953-349-26677 | Sequence 26677, A |
| 33 | 7 | 1.0 | 467 | US-10-511-937-2961 | Sequence 2961, Ap |
| 34 | 7 | 1.0 | 467 | US-10-953-349-26676 | Sequence 26676, A |
| 35 | 7 | 1.0 | 470 | US-10-953-349-37511 | Sequence 37511, A |
| 36 | 7 | 1.0 | 476 | US-10-953-349-8751 | Sequence 8751, Ap |
| 37 | 7 | 1.0 | 476 | US-10-953-349-26675 | Sequence 26675, A |
| 38 | 7 | 1.0 | 518 | US-10-953-349-32100 | Sequence 32100, A |
| 39 | 7 | 1.0 | 557 | US-10-953-349-7230 | Sequence 7230, Ap |
| 40 | 7 | 1.0 | 557 | US-10-953-349-11010 | Sequence 11010, A |
| 41 | 7 | 1.0 | 562 | US-10-953-349-7229 | Sequence 7229, Ap |
| 42 | 7 | 1.0 | 570 | US-10-953-349-11009 | Sequence 11009, A |
| 43 | 7 | 1.0 | 3010 | US-11-140-487A-769 | Sequence 769, App |
| 44 | 7 | 1.0 | 3010 | US-11-140-487A-770 | Sequence 770, App |
| 45 | 6 | 0.9 | 20 | US-11-251-465-99 | Sequence 99, Appl |

ALIGNMENTS

RESULT 1
US-10-196-749-150
Sequence 150, Application US/10196749
Publication No. US200609486441
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196, 749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 150
LENGTH: 678
TYPE: PRT
ORGANISM: Homo Sapien
US-10-196-749-150

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-11-101-316-34
; Sequence 34, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P323ORIC17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; PRIOR FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 34
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-34

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 4497, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4497
LENGTH: 503
TYPE: PRT
ORGANISM: Homo sapiens
US-11-293-697-4497

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 373 SICKRRR 380

RESULT 4

US-10-196-749-46
Sequence 46: Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gueney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196,749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
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PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-10-24
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PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
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SEQ ID NO 46
LENGTH: 550
TYPE: PRT
ORGANISM: Homo Sapien
US-10-196-749-46

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Db 372 IDGSSSVG 379

RESULT 5

US-10-953-349-36732
Sequence 36732: Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 36732
LENGTH: 91
TYPE: PRT
ORGANISM: Zea mays subsp. mays
US-10-953-349-36732

Query Match 1.0%; Score 7; DB 6; Length 91;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 203 PPSAAS 209
Db 17 PPSAAS 23

RESULT 6

US-10-953-349-37027
Sequence 37027: Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 37027
LENGTH: 99
TYPE: PRT
ORGANISM: Zea mays subsp. mays
US-10-953-349-37027

Query Match 1.0%; Score 7; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 LVTGVHS 26
Db 79 LVTGVHS 85

RESULT 7

US-10-953-349-30530
Sequence 30530: Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
ENCODDED THEREBY

```

; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30530
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-10-953-349-30530
```

```

Query Match          1.0%; Score 7; DB 6; Length 126;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      251 DPGAAF 257
        |||||
Db       29 DPGAAF 35
```

```

RESULT 8
US-10-953-349-37026
```

```

; Sequence 37026, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37026
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37026
```

```

Query Match          1.0%; Score 7; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      20 LVTGVHS 26
        |||||
Db       108 LVTGVHS 114
```

```

RESULT 9
```

```

US-10-953-349-37025
; Sequence 37025, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37025
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37025
```

```

Query Match          1.0%; Score 7; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      20 LVTGVHS 26
        |||||
```

```
Db       122 LVTGVHS 128
```

```

RESULT 10
```

```

US-10-953-349-30529
; Sequence 30529, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30529
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-10-953-349-30529
```

```

Query Match          1.0%; Score 7; DB 6; Length 170;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      251 DPGAAF 257
        |||||
Db       73 DPGAAF 79
```

```

RESULT 11
```

```

US-10-953-349-28247
; Sequence 28247, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28247
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-10-953-349-28247
```

```

Query Match          1.0%; Score 7; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      208 ASTTSIP 214
        |||||
Db       92 ASTTSIP 98
```

```

RESULT 12
```

```

US-10-953-349-30528
; Sequence 30528, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30528
```

LENGTH: 202
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-953-349-30528

Query Match 1.0%; Score 7; DB 6; Length 202;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 DPGSAF 257
|||
Db 105 DPGSAF 111

RESULT 13
US-10-953-349-31820
Sequence 31820, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31820
LENGTH: 217
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-953-349-31820

Query Match 1.0%; Score 7; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 AVTVAVA 195
|||
Db 155 AVTVAVA 161

RESULT 14
US-10-953-349-18707
Sequence 18707, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18707
LENGTH: 246
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-18707

Query Match 1.0%; Score 7; DB 6; Length 246;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 SAASTTS 212
|||
Db 127 SAASTTS 133

RESULT 15
US-10-953-349-31819
Sequence 31819, Application US/10953349

Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31819
LENGTH: 247
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-953-349-31819

Query Match 1.0%; Score 7; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 AVTVAVA 195
|||
Db 185 AVTVAVA 191

Search completed: June 7, 2006, 01:59:31
Job time : 17 secs

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